Atty. Docket No.: 8039/1090 PATENT

IN THE UNITED STATES PATENT AND TRADEMARK OFFICE

Application of:	Riechmann, et al.	Examiner:	B. Celsa
Serial No.:	09/710,444		
Filed:	November 10, 2000	Group Art Unit:	1639
Entitled:	Selection System		
		Conf. No.:	5253

#17

CERTIFICATE OF MAILING UNDER 37 C.F.R. § 1.8a

I hereby certify that this correspondence (and any paper or fee referred to as being enclosed) is being deposited with the United States Post Office as First Class Mail on the date indicated below in an envelope addressed to Commissioner for Patents, P.O. Box 1450, Alexandria, VA 22313-1450.

Kathleen Williams
Name of Person Mailing Paper

Signature of Person Mailing Paper

Commissioner for Patents
P.O. Box 1450
Alexandria, VA 22313-1450

REQUEST UNDER 37 C.F.R. §1.181 TO WITHDRAW HOLDING OF ABANDONMENT

Sir:

Applicants hereby request withdrawal of the holding of abandonment announced in the Notice of Abandonment mailed September 22, 2003.

This is filed in response to the Notice of Abandonment of Non-Provisional Application mailed by the US Patent & Trademark Office on September 22, 2003.

The Notice stated that Applicants failed to comply with the Sequence Rules within 6 months of the first letter, dated February 27, 2002, and within 1 month of the Non-bona fide response letter dated March 17, 2003. Applicants submit that bona fide responses to both communications from the Patent Office were timely filed and that the holding of abandonment is in error. This assertion is supported as follows. Enclosed are the following:

1) A copy of the Notice to Comply mailed February 27, 2002;

2) A copy of the response filed July 25, 2002, including fee and petition for Extension of Time. This response included paper and diskette copies of the sequence listing and the required statement under 37 CFR §1.821 (f) and (g);

3) A copy of the second Notice to Comply (Non-bona fide). That notice stated that the disk was melted by the U.S.P.T.O. and set a 1 month non-extendable deadline for response. Applicants note that the response was properly mailed to the Arlington, VA address established for Sequence Diskette Submission to avoid irradiation damage to the diskette;

4) A copy of the filing of April 8, 2003, responsive to the March 17,2003 communication. That filing included a new diskette, paper copy of the Sequence Listing and Statement under 37 C.F.R. 1.821 (f) and (g) and a return postcard. Applicants submit that the April 8, 2003 filing was well within the 1 month time set in the second Notice to Comply; and

5) A copy of the O I.P.E.-stamped copy of the return postcard filed with the April 8, 2003 response to the second Notice to Comply. The filing was stamped by the U.S.P.T.O. on April 11, 2003. The return of the date-stamped postcard acknowledges receipt of all items asked for in the second Notice to Comply: a substitute diskette; a substitute paper copy of the Sequence Listing; and a Statement Under 37 CFR 1.821 (f) and (g).

In view of the above, Applicants submit that Applicants have fully and timely responded to all Notices from the U.S.P.T.O. Applicants therefore respectfully request notice that the holding of abandonment has been withdrawn.

Because it is believed that the Notice of Abandonment is in error, it is believed that no fees are due with this filing. However, the Commissioner for Patents is authorized to charge all fees in the total amount to Deposit Account No. 16-0085, Reference 8039/1090.

Respectfully submitted,

Date: 9/26/03

Name: Kathleen Williams
Registration No.: 34,380
Customer No.: 29933
Palmer & Dodge LLP
111 Huntington Avenue
Boston, MA 02199-7613
Tel: 617-239-0100

Atty. Docket No.: 8039/1090 PATENT

IN THE UNITED STATES PATENT AND TRADEMARK OFFICE

Application of:	Riechmann, et al.	Examiner:	B. Celsa
Serial No.:	09/710,444		
Filed:	November 10, 2000	Group Art Unit:	1639
Entitled:	Selection System		
		Conf. No.:	5253

CERTIFICATE OF MAILING UNDER 37 C.F.R. § 1.8a

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Kathleen Williams
Name of Person Mailing Paper

Signature of Person Mailing Paper

Commissioner for Patents
P.O. Box 1450
Alexandria, VA 22313-1450

TRANSMITTAL LETTER

Enclosed for filing the above-identified patent application, please find the following documents:

1. Request Under 37. C.F.R. §1.181 to Withdraw Holding of Abandonment;
2. Copy of the Office Action Mailed February 27, 2002;
3. Copy of the Response to the 2/27/02 Office Action (filed 7/25/02).
4. Copy of the Office Action mailed 3/17/03;
5. Copy of the Response to the 3/17/03 Office Action (filed April 8, 2003).
6. Copy of the O.I.P.E.-stamped copy of the Return Post Card filed with the April 8, 2003 Response to the Second Notice to Comply; and
7. Return Post Card.

The Commissioner for Patents is hereby authorized to charge any additional fees or credit any overpayment in the total fees to Deposit Account No. 16-0085, Reference 8039/1090. A duplicate of this transmittal letter is enclosed for this purpose.

Respectfully submitted,

Date: 9/26/03

Name: Kathleen Williams
Registration No.: 34,380
Customer No.: 29933
Palmer & Dodge LLP
111 Huntington Avenue
Boston, MA 02199-7613
Tel: 617-239-0100

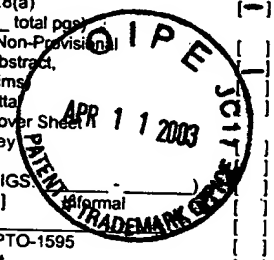
Serial No. 09/710,444 File No. 8039/1090 By: (MBW) KMW

Applicant(s): Riechmann, et al.

Title: Selection System

The Following, DUE _____ in the USPTO, was received by the PTO Mail Room on the date stamped hereon:

[ ] Cert. of Mailing by Express Mail (37 CFR 1.10)
Express Mail Label No. _____
[ ] Cert. of Mailing under 37 CFR 1.8(a)
[ ] Patent Application (_____ total pgs)
[ ] Provisional or [ ] Non-Provisional
(pgs) Specification (pgs) Abstract,
(pgs) Claims (_____ # claims)
[ ] New Patent Application Transmittal
[ ] Provisional Patent Application Cover Sheet
[ ] Declaration and Power of Attorney
[ ] Application Data Sheet
[ ] Drawings _____ Sheet(s) (FIGS. _____ - _____)
[ ] Formal or [ ] Informal
[ ] Assignment of _____
[ ] Recordation Cover Sheet Form PTO-1595
[ ] Information Disclosure Statement
[ ] Form PTO 1449 and Copies of Cited References



[ ] Response to Notice to File Missing Parts
[ ] Copy of Part 2 of NFMP
[X] Diskette Containing Nucleotide and/or Amino Acid Sequence Listing Substitute
[ ] Priority Document(s) # _____
[ ] Amendment/Response
[ ] Petition for Extension of Time (x2)
[ ] Check in the amount of _____
Check # _____
[ ] Transmittal of Formal Drawings
[ ] Motion/Opposition/Reply
[ ] Request for Cont'd Examination (RCE)
[ ] Notice of Appeal
[ ] Appeal Brief (x3)
[ ] Issue Fee Transmittal
[X] Transmittal Letter (x2)

[X] Other Substitute Paper Copy of the Sequence Listing; Copy of Notice to Comply; Statement Under 37 CFR 1.821(f) & (g)

MAILED April 8, 2003

RECEIVED
APR 17 2003
PATENT DEPT.
PALMER & DODGE LLP

UNITED STATES PATENT AND TRADEMARK OFFICE

UNITED STATES DEPARTMENT OF COMMERCE
United States Patent and Trademark Office
Address: COMMISSIONER OF PATENTS AND TRADEMARKS
Washington, D.C. 20231
www.uspto.gov

APPLICATION NO.	FILING DATE	FIRST NAMED INVENTOR	ATTORNEY DOCKET NO.	CONFIRMATION NO.
09/710,444	11/10/2000	Lutz Riechmann	8654/1090	5253

29933 7590 03/17/2003

PALMER & DODGE, LLP
KATHLEEN M. WILLIAMS
111 HUNTINGTON AVENUE
BOSTON, MA 02199

EXAMINER	
CELSA, BENNETT M	

ART UNIT	PAPER NUMBER
1639	

DATE MAILED: 03/17/2003

13

Please find below and/or attached an Office communication concerning this application or proceeding.

Docketed Doreen
Response Due Notice to Comply
Statutory Period 4/17/03-FINAL
Palmer & Dodge LLP Non-Extendible
Patent Department

UNITED STATES DEPARTMENT OF COMMERCE
Patent and Trademark Office
COMMISSIONER OF PATENTS AND TRADEMARKS
Washington, D.C. 20231

SERIAL NUMBER	FILING DATE	FIRST NAMED APPLICANT	ATTORNEY DOCKET NO.
09/ 710,444			

EXAMINER	
ART UNIT	PAPER NUMBER
1639	13

Please find below a communication from the EXAMINER in charge of this application

NOTICE TO COMPLY: SEQUENCE RULES (NONBONAFIDE)

1. Applicant's submission of a computer readable form (CRF) and corresponding paper sequence listing in paper no. 12 (dated 12/10/02) is acknowledged.

However, this application fails to comply with the requirements of 37 CFR 1.821 through 1.825 for the reason(s) set forth on the attached Notice To Comply With Requirements For Patent Applications Containing Nucleotide Sequence And/Or Amino Acid Sequence Disclosures and **CRF PROBLEM REPORT**. Applicant must comply with the requirements of the sequence rules (37 CFR 1.821 - 1.825) before the application can be examined under 35 U.S.C. §§ 131 and 132.

Applicant is given ONE MONTH (NON-EXTENDIBLE) from the mailing date of this communication within which to COMPLY WITH THE SEQUENCE RULES, 37 CFR 1.821 - 1.825. Failure to comply with these requirements will result in ABANDONMENT of the application. Direct the reply to the undersigned. Applicant is requested to return a copy of the attached Notice to Comply with the reply.

Any inquiry concerning this communication or earlier communications from the examiner should be directed to Examiner Celsa whose telephone number is (703) 305-7556). If the examiner cannot be reached, inquiries can be directed to Supervisory Patent Examiner Andrew Wang whose telephone number is (703) 306-3217. Inquiry of a general nature or relating to the status of this application should be directed to the Group receptionist whose telephone number is (703) 308-0196.

Primary Examiner Celsa
ART UNIT 1639

March 14, 2003

BENNETT CELSA
PRIMARY EXAMINER

Application No.: 10/710,444

NOTICE TO COMPLY WITH REQUIREMENTS FOR PATENT APPLICATIONS CONTAINING NUCLEOTIDE SEQUENCE AND/OR AMINO ACID SEQUENCE DISCLOSURES

Applicant must file the items indicated below within the time period set the Office action to which the Notice is attached to avoid abandonment under 35 U.S.C. § 133 (extensions of time may be obtained under the provisions of 37 CFR 1.136(a)).

The nucleotide and/or amino acid sequence disclosure contained in this application does not comply with the requirements for such a disclosure as set forth in 37 C.F.R. 1.821 - 1.825 for the following reason(s):

- [X] 1. This application clearly fails to comply with the requirements of 37 C.F.R. 1.821-1.825. Applicant's attention is directed to the final rulemaking notice published at 55 FR 18230 (May 1, 1990), and 1114 OG 29 (May 15, 1990). If the effective filing date is on or after July 1, 1998, see the final rulemaking notice published at 63 FR 29620 (June 1, 1998) and 1211 OG 82 (June 23, 1998).
- [ ] . This application does not contain, as a separate part of the disclosure on paper copy, a "Sequence Listing" as required by 37 C.F.R. 1.821(c).
- [ ] 3. A copy of the "Sequence Listing" in computer readable form has not been submitted as required by 37 C.F.R. 1.821(e).
- [ ] . A copy of the "Sequence Listing" in computer readable form has been submitted. However, the content of the computer readable form does not comply with the requirements of 37 C.F.R. 1.822 and/or 1.823, as indicated on the attached copy of the marked -up "Raw Sequence Listing."
- [X] 5. The computer readable form that has been filed with this application has been found to be damaged and/or unreadable as indicated on the attached CRF Diskette Problem Report. A Substitute computer readable form must be submitted as required by 37 C.F.R. 1.825(d).
- [ ] 6. The paper copy of the "Sequence Listing" is not the same as the computer readable from of the "Sequence Listing" as required by 37 C.F.R. 1.821(e).
- [ ] . Other:

Applicant Must Provide:

- [X] An initial or **substitute** computer readable form (CRF) copy of the "Sequence Listing".
- [X] An initial or **substitute** paper copy of the "Sequence Listing", as well as an amendment directing its entry into the specification.
- [X] A statement that the content of the paper and computer readable copies are the same and, where applicable, include no new matter, as required by 37 C.F.R. 1.821(e) or 1.821(f) or 1.821(g) or 1.825(b) or 1.825(d).

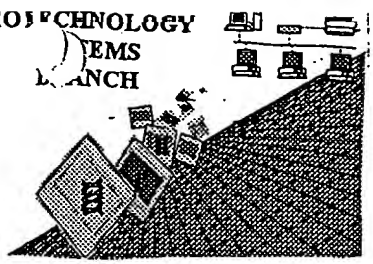
For questions regarding compliance to these requirements, please contact:

For Rules Interpretation, call (703) 308-4216
For CRF Submission Help, call (703) 308-4212
PatentIn Software Program Support
Technical Assistance.....703-287-0200
To Purchase PatentIn Software.....703-306-2600

PLEASE RETURN A COPY OF THIS NOTICE WITH YOUR REPLY

1600

1637



CRF Problem Report

The Scientific and Technical Information Center (STIC) experienced a problem when processing the following computer readable form (CRF):

#12

Application Serial Number: 09/710,444A
Filing Date: 11/10/2000
Date Processed by STIC: 11/29/02

STIC Contact: **Mark Spencer, 703-308-4212**

Nature of Problem:

The CRF (was):

Melted

__✓__ (circle one) Damaged or Unreadable (for Unreadable, see attached)
____ Blank (no files on CRF) (see attached)
____ Empty file (filename present, but no bytes in file) (see attached)
____ Virus-infected. Virus name: _____ The STIC will not process the CRF.
____ Not saved in ASCII text
____ Sequence Listing was embedded in the file. According to Sequence Rules, submitted file should **only** be the Sequence Listing.
____ Did not contain a Sequence Listing. (see attached sample)
____ Other:

_____

PLEASE USE THE CHECKER VERSION 3.1 PROGRAM TO REDUCE ERRORS. SEE BELOW FOR ADDRESS:

http:/www.uspto.gov/web/offices/pac/checker

Applicants submitting genetic sequence information electronically on diskette or CD-Rom should be aware that there is a possibility that the disk/CD-Rom may have been affected by treatment given to all incoming mail. Please consider using alternate methods of submission for the disk/CD-Rom or replacement disk/CD-Rom. Any reply including a sequence listing in electronic form should NOT be sent to the 20231 zip code address for the United States Patent and Trademark Office, and instead should be sent via the following to the indicated addresses:

1. EFS-Bio (<http://www.uspto.gov/ebc/efs/downloads/documents.htm>, **EFS Submission User Manual** - ePAVE)
2. **U.S. Postal Service:** U.S. Patent and Trademark Office, Box Sequence, P.O. Box 2327, Arlington, VA 22202
3. **Hand Carry directly to:**
   U.S. Patent and Trademark Office, Technology Center 1600, Reception Area, 7th Floor, Examiner Name, Sequence Information, Crystal Mall One, 1911 South Clark Street, Arlington, VA 22202
   Or
   U.S. Patent and Trademark Office, Box Sequence, Customer Window, Lobby, Room 1B03, Crystal Plaza Two, 2011 South Clark Place, Arlington, VA 22202
4. **Federal Express, United Parcel Service, or other delivery service to:** U.S. Patent and Trademark Office, Box Sequence, Room 1B03-Mailroom, Crystal Plaza Two, 2011 South Clark Place, Arlington, VA 22202

Revised 01/29/2002

UNITED STATES PATENT AND TRADEMARK OFFICE

UNITED STATES DEPARTMENT OF COMMERCE
United States Patent and Trademark Office
Address: COMMISSIONER OF PATENTS AND TRADEMARKS
Washington, D.C. 20231
www.uspto.gov

APPLICATION NO.	FILING DATE	FIRST NAMED INVENTOR	ATTORNEY DOCKET NO.	CONFIRMATION NO.
09/710,444	11/10/2000	Lutz Riechmann	8654/1090	5253

7590 02/27/2002

Palmer & Dodge LLP
One Beacon Street
Boston, MA 02109-3190

EXAMINER	
CELSA, BENNETT M	
ART UNIT	PAPER NUMBER
1627	

DATE MAILED: 02/27/2002

Please find below and/or attached an Office communication concerning this application or proceeding.

Docket # Doreen
Response due Notice to Comply
Statutory period 3/27/02 (8/27/02
Palmer & Dodge LLP Drop Dead Date)
Patent Department

UNITED STATES DEPARTMENT OF COMMERCE
Patent and Trademark Office
COMMISSIONER OF PATENTS AND TRADEMARKS
Washington, D.C. 20231

SERIAL NUMBER	FILING DATE	FIRST NAMED APPLICANT	ATTORNEY DOCKET NO.
09/ 710,444			

EXAMINER	
ART UNIT	PAPER NUMBER
1627	5

Please find below a communication from the EXAMINER in charge of this application

Sequence Rule Compliance: NOTICE TO COMPLY

This application fails to comply with the sequence rule quirements of 37 C.F.R. §§ 1.821-1.825 for the reason(s) set forth on the attached Notice To Comply With Requirements For Patent Applications Containing Nucleotide Sequence And/Or Amino Acid Sequence Disclosures. This application **encompasses sequences needing sequence identifiers (e.g. see pages 9, 15, 24, 30, 35, 36, 38, figures etc.).**

APPLICANT IS GIVEN 30 days FROM THE DATE OF THIS LETTER WITHIN WHICH TO COMPLY WITH THE SEQUENCE RULES, 37 C.R.F. §§ 1.821-1.825. Failure to comply with these requirements will result in ABANDONMENT of the application under 37 C.F.R. § 1.821(g). Extensions of time may be obtained by filing a petition accompanied by the extension fee under the provisions of 37 C.F.R. § 1.136. In no case may an applicant extend the period for response beyond the six month statutory period. Direct the response to the undersigned. Applicant is requested to return a copy of the attached Notice to Comply with the response.

Any inquiry concerning this communication or earlier communications from the examiner should be directed to Examiner Celsa whose telephone number is (703) 305-7556 If the examiner cannot be reached, inquiries can be directed to Supervisory Patent Examiner Venkat whose telephone number is (703) 308-0570. The fax number for the organization where this application or proceeding is assigned is (703) 308-4242. Any inquiry of a general nature or relating to the status of this application should be directed to the Group receptionist whose telephone number is (703) 308-0196.

Bennett Celsa (au 1627) (Feb. 25,2002)

BENNETT CELSA
PRIMARY EXAMINER

Application No. 09/710,444

NOTICE TO COMPLY WITH REQUIREMENTS FOR PATENT APPLICATIONS CONTAINING NUCLEOTIDE SEQUENCE AND/OR AMINO ACID SEQUENCE DISCLOSURES

The nucleotide and/or amino acid sequence disclosure contained in this application does not comply with the requirements for such a disclosure as set forth in 37 CFR 1.821 - 1.825 for the following reason(s):

☒ 1. This application clearly fails to comply with the requirements of 37 CFR 1.821 - 1.825. Applicant's attention is directed to these regulations, published at 1114 OG 29, May 15, 1990 and at 55 FR 18230, May 1, 1990.

☒ 2. This application does not contain, as a separate part of the disclosure on paper copy, a "Sequence Listing" as required by 37 CFR 1.821(c).

☒ 3. A copy of the "Sequence Listing" in computer readable form has not been submitted as required by 37 CFR 1.821

☐ 4. A copy of the "Sequence Listing" in computer readable form has been submitted. However, the content of the computer readable form does not comply with the requirements of 37 CFR 1.822 and/or 1.823, as indicated on the attached marked-up copy of the "Raw Sequence Listing."

☐ 5. The computer readable form that has been filed with this application has been found to be damaged and/or unreadable as indicated on the attached CRF Diskette Problem Report. A substitute computer readable form must be submitted as required by 37 CFR 1.825(d).

☐ 6. The paper copy of the "Sequence Listing" is not the same as the computer readable form of the "Sequence Listing" as required by 37 CFR 1.821(e).

☐ 7. Other: _____

Applicant must provide:

☒ An initial ~~or substitute~~ computer readable form (CRF) copy of the "Sequence Listing"

☒ An initial ~~or substitute~~ paper copy of the "Sequence Listing", as well as an amendment directing its entry into the specification

☒ A statement that the content of the paper and computer readable copies are the same and, where applicable, include no new matter, as required by 37 CFR 1.821(e) or 1.821(f) or 1.821(g) or 1.825(b) or 1.825(d)

For questions regarding compliance with these requirements, please contact:

For Rules Interpretation, call (703) 308-1123
For CRF submission help, call (703) 308-4212
For PatentIn software help, call (703) 308-6856

Please return a copy of this notice with your response.

Attachment for PTO-948 (Rev. 03/01, or earlier)
6/18/01

The below text replaces the pre-printed text under the heading, "Information on How to Effect Drawing Changes," on the back of the PTO-948 (Rev. 03/01, or earlier) form.

INFORMATION ON HOW TO EFFECT DRAWING CHANGES

1. Correction of Informalities -- 37 CFR 1.85

New corrected drawings must be filed with the changes incorporated therein. Identifying indicia, if provided, should include the title of the invention, inventor's name, and application number, or docket number (if any) if an application number has not been assigned to the application. If this information is provided, it must be placed on the front of each sheet and centered within the top margin. If corrected drawings are required in a Notice of Allowability (PTOL-37), the new drawings **MUST** be filed within the **THREE MONTH** shortened statutory period set for reply in the Notice of Allowability. Extensions of time may NOT be obtained under the provisions of 37 CFR 1.136(a) or (b) for filing the corrected drawings after the mailing of a Notice of Allowability. The drawings should be filed as a separate paper with a transmittal letter addressed to the Official Draftsperson.

2. Corrections other than Informalities Noted by Draftsperson on form PTO-948.

All changes to the drawings, other than informalities noted by the Draftsperson, **MUST** be made in the same manner as above except that, normally, a highlighted (preferably red ink) sketch of the changes to be incorporated into the new drawings **MUST** be approved by the examiner before the application will be allowed. No changes will be permitted to be made, other than correction of informalities, unless the examiner has approved the proposed changes.

Timing of Corrections

Applicant is required to submit the drawing corrections within the time period set in the attached Office communication. See 37 CFR 1.85(a).

Failure to take corrective action within the set period will result in **ABANDONMENT** of the application.

Atty. Docket No.: 8039/1090 **PATENT**

IN THE UNITED STATES PATENT AND TRADEMARK OFFICE

Application of:	Riechmann, et al.	Examiner:	B. Celsa
Serial No.:	09/710,444		
Filed:	November 10, 2000	Group Art Unit:	1639
Entitled:	"Selection System"		
		Conf. No.:	5253

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Mary Wilson
Name of Person Mailing Paper

Signature of Person Mailing Paper

U.S. Patent & Trademark Office
Box: Sequence
PO Box 2327
Arlington, VA 22202

TRANSMITTAL LETTER

Enclosed for filing the above-identified patent application, please find the following documents:

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2. Copy of Notice to Comply;
3. Substitute Paper Copy of the Sequence Listing;
4. Substitute Computer Readable Copy of the Sequence Listing;
5. Statement Under 37 C.F.R. §1.821(f) and (g); and
6. Return Post Card.

It is believed that no fees are due. However, if necessary, the Commissioner for Patents is hereby authorized to charge all fees in the total amount to Deposit Account No. 16-0085, Reference 8039/1090. A duplicate of this transmittal letter is enclosed for this purpose.

Respectfully submitted,

Date: April 8, 2003

Name: Mark J. FitzGerald
Registration No.: 45,928
Palmer & Dodge LLP
111 Huntington Avenue
Boston, MA 02199-7613
Tel: 617-239-0100

~~Docket #~~
Response due
Statutory period
Palmer & Dodge LLP
Patent Department

Atty. Docket No.: 8039/1090 **PATENT**

IN THE UNITED STATES PATENT AND TRADEMARK OFFICE

Application of:	Riechmann, et al.	Examiner:	B. Celsa
Serial No.:	09/710,444		
Filed:	November 10, 2000	Group Art Unit:	1639
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Mary Wilson
Name of Person Mailing Paper

Signature of Person Mailing Paper

U.S. Patent & Trademark Office
Box: Sequence
PO Box 2327
Arlington, VA 22202

TRANSMITTAL LETTER

Enclosed for filing the above-identified patent application, please find the following documents:

1. Response to Office Action mailed March 17, 2003;
2. Copy of Notice to Comply;
3. Substitute Paper Copy of the Sequence Listing;
4. Substitute Computer Readable Copy of the Sequence Listing;
5. Statement Under 37 C.F.R. §1.821(f) and (g); and
6. Return Post Card.

It is believed that no fees are due. However, if necessary, the Commissioner for Patents is hereby authorized to charge all fees in the total amount to Deposit Account No. 16-0085, Reference 8039/1090. A duplicate of this transmittal letter is enclosed for this purpose.

Respectfully submitted,

Date: April 8, 2003

Name: Mark J. FitzGerald
Registration No.: 45,928
Palmer & Dodge LLP
111 Huntington Avenue
Boston, MA 02199-7613
Tel: 617-239-0100

Application No.: 10/0,444

NOTICE TO COMPLY WITH REQUIREMENTS FOR PATENT APPLICATIONS CONTAINING NUCLEOTIDE SEQUENCE AND/OR AMINO ACID SEQUENCE DISCLOSURES

Applicant must file the items indicated below within the time period set the Office action to which the Notice is attached to avoid abandonment under 35 U.S.C. § 133 (extensions of time may be obtained under the provisions of 37 CFR 1.136(a)).

The nucleotide and/or amino acid sequence disclosure contained in this application does not comply with the requirements for such a disclosure as set forth in 37 C.F.R. 1.821 - 1.825 for the following reason(s):

- [X] 1. This application clearly fails to comply with the requirements of 37 C.F.R. 1.821-1.825. Applicant's attention is directed to the final rulemaking notice published at 55 FR 18230 (May 1, 1990), and 1114 OG 29 (May 15, 1990). If the effective filing date is on or after July 1, 1998, see the final rulemaking notice published at 63 FR 29620 (June 1, 1998) and 1211 OG 82 (June 23, 1998).
- [ ] . This application does not contain, as a separate part of the disclosure on paper copy, a "Sequence Listing" as required by 37 C.F.R. 1.821(c).
- [ ] 3. A copy of the "Sequence Listing" in computer readable form has not been submitted as required by 37 C.F.R. 1.821(e).
- [ ] . A copy of the "Sequence Listing" in computer readable form has been submitted. However, the content of the computer readable form does not comply with the requirements of 37 C.F.R. 1.822 and/or 1.823, as indicated on the attached copy of the marked -up "Raw Sequence Listing."
- [X] 5. The computer readable form that has been filed with this application has been found to be damaged and/or unreadable as indicated on the attached CRF Diskette Problem Report. A Substitute computer readable form must be submitted as required by 37 C.F.R. 1.825(d).
- [ ] 6. The paper copy of the "Sequence Listing" is not the same as the computer readable from of the "Sequence Listing" as required by 37 C.F.R. 1.821(e).
- [ ] . Other:

Applicant Must Provide:

- [X] An initial or **substitute** computer readable form (CRF) copy of the "Sequence Listing".
- [X] An initial or **substitute** paper copy of the "Sequence Listing", as well as an amendment directing its entry into the specification.
- [X] A statement that the content of the paper and computer readable copies are the same and, where applicable, include no new matter, as required by 37 C.F.R. 1.821(e) or 1.821(f) or 1.821(g) or 1.825(b) or 1.825(d).

For questions regarding compliance to these requirements, please contact:

For Rules Interpretation, call (703) 308-4216
~~For CRF Submission Help, call (703) 308-4212~~
PatentIn Software Program Support
Technical Assistance.....703-287-0200
To Purchase PatentIn Software.....703-306-2600

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Atty. Docket No.: 8039/1090 **PATENT**

IN THE UNITED STATES PATENT AND TRADEMARK OFFICE

Application of:	Riechmann, et al.	Examiner:	B. Celsa
Serial No.:	09/710,444		
Filed:	November 10, 2000	Group Art Unit:	1639
Entitled:	"Selection System"		
		Conf. No.:	5253

CERTIFICATE OF MAILING UNDER 37 C.F.R. § 1.8a

I hereby certify that this correspondence (and any paper or fee referred to as being enclosed) is being deposited with the United States Post Office as First Class Mail on the date indicated below in an envelope addressed to: U.S. Patent & Trademark Office, Box: Sequence, P.O. Box 2327, Arlington, VA 22202.

Mary Wilson
Name of Person Mailing Paper

Signature of Person Mailing Paper

U.S. Patent and Trademark Office
Box: Sequence
P.O. Box 2327
Arlington, VA 22202

RESPONSE TO OFFICE ACTION

Sir:

This is filed in response to the Office Action of Non-Provisional Application mailed March 17, 2003 in the above-noted U.S. patent application.

The Office Action stated that the Applicant must provide substitute computer readable and paper copies of the sequence listing along with the sequence listing statement required under 37 C.F.R. §1.821(f) and (g), because the disk submitted December 10, 2002 was damaged by the P.T.O.

Enclosed please find a Substitute paper copy of the Sequence Listing, a Substitute Computer Readable copy of the Sequence Listing, and the Statement Under 37 C.F.R. §1.821(f) and (g).

It is believed that no fees are due. However, if necessary, the Commissioner for Patents is hereby authorized to charge all fees in the total amount to Deposit Account No. 16-0085, Reference 8039/1090. A duplicate of this transmittal letter is enclosed for this purpose.

Respectfully submitted,

Date: April 8, 2003

Name: Mark J. FitzGerald
Registration No.: 45,928
Palmer & Dodge LLP
111 Huntington Avenue
Boston, MA 02199-7613
Tel: 617-239-0100

Atty. Docket No.: 8039/1090 PATENT

IN THE UNITED STATES PATENT AND TRADEMARK OFFICE

Application of:	Riechmann, et al.	Examiner:	B. Celsa
Serial No.:	09/710,444		
Filed:	November 10, 2000	Group Art Unit:	1639
Entitled:	"Selection System"		
		Conf. No.:	5253

CERTIFICATE OF MAILING UNDER 37 C.F.R. § 1.8a

I hereby certify that this correspondence (and any paper or fee referred to as being enclosed) is being deposited with the United States Post Office as First Class Mail on the date indicated below in an envelope addressed to: U.S. Patent & Trademark Office, Box: Sequence, P.O. Box 2327, Arlington, VA 22202.

Mary Wilson
Name of Person Mailing Paper

Signature of Person Mailing Paper

U.S. Patent & Trademark Office
Box: Sequence
PO Box 2327
Arlington, VA 22202

STATEMENT UNDER 37 C.F.R. §1.821(f) and (g)

Sir:

This paper is submitted in response to the Office Action mailed by the USPTO on March 17, 2003.

In accordance with 37 C.F.R. §1.821 (f) I hereby state that the paper copy and the computer readable form of the Sequence Listing submitted herewith in the above-identified patent application are supported in the application and contain no new matter. I hereby state that the information recorded in computer readable form is identical to the written sequence listing.

In accordance with 37 C.F.R. §1.821 (g), I hereby state that the computer readable form of the Sequence Listing submitted herewith contains no new matter.

Respectfully submitted,

Date: April 8, 2003

Name: Mark J. FitzGerald
Registration No.: 45,928
Palmer & Dodge LLP
111 Huntington Avenue
Boston, MA 02199-7613
Tel: 617-239-0100

SEQUENCE LISTING

<110> Riechmann, Lutz

Kristensen, Peter

Jestin, Jean-Luc

Winter, Gregory

<120> Selection System

<130> 8039/1090

<140> 09/710,444

<141> 2000-11-20

<150> GB 9810223.9

<151> 1998-05-13

<150> GB 9810228.8

<151> 1998-05-13

<150> PCT/GB99/01526

<151> 1999-05-13

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<222> (97)..(97)

<223> n at position 97 can be G, A, T or C

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<223> n at position 38 can be G, A, T or C.

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<222> (42)..(42)

<223> n at position 42 can be G, A, T or C.

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<222> (43)..(43)

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Ala Gln Pro Ala Met Ala
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Ala Gln Pro Ala Met Ala
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Val Gln Pro Ala Met Ala
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<211> 18

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agment of Thermus aquaticus DNA polymerase I

<400> 47

tttcgcaaga tgtggcgt 18

<210> 48

<211> 12

<212> DNA

<213> Artificial sequence

<220>

<223> Synthetic oligonucleotide primer used as a substrate for Thermus
aquaticus DNA polymerase I.

<220>

<221> misc_feature

<222> (1)..(12)

<223> Synthetic primer used as substrate for Stoffel fragment of Thermu
s aquaticus DNA polymerase I

<400> 48

gcgaagatgt gg 12

<210> 49

<211> 30

<212> DNA

<213> Artificial sequence

<220>

<223> Synthetic oligonucleotide primer used as a substrate for Thermus aquaticus DNA polymerase I.

<220>

<221> misc_feature

<222> (1)..(30)

<223> Synthetic oligonucleotide primer used as substrate for Thermus aq uaticus DNA polymerase I

<400> 49

aaatacaaca ataaaacgcc acatcttgcg 30

<210> 50

<211> 20

<212> DNA

<213> Artificial sequence

<220>

<223> Synthetic oligonucleotide sequence insert containing PstI restric

tion site and frame shift for H102A mutant barnase fusion construct fused to p3 gene of phage fd-3.

<220>

<221> misc_feature

<222> (1)..(20)

<223> Synthetic oligonucleotide sequence insert containing PstI restriction site and frame shift for H102A mutant barnase fusion construct fused to p3 gene of phage fd-3.

<400> 50

ctgcaggcgg tgcggccgca 20

<210> 51

<211> 24

<212> DNA

<213> Artificial sequence

<220>

<223> Synthetic oligonucleotide used for random priming.

<220>

<221> misc_feature

<222> (1)..(24)

<223> Synthetic oligonucleotide used for random priming

<220>

<221> misc_feature

<222> (19)..(19)

<223> n at position 19 can be G, A, T or C.

<220>

<221> misc_feature

<222> (20)..(20)

<223> n at position 20 can be G, A, T or C.

<220>

<221> misc_feature

<222> (21)..(21)

<223> n at position 21 can be G, A, T or C.

<220>

<221> misc_feature

<222> (22)..(22)

<223> n at position 22 can be G, A, T or C.

<220>

<221> misc_feature

<222> (23)..(23)

<223> n at position 23 can be G, A, T or C.

<220>

<221> misc_feature

<222> (24)..(24)

<223> n at position 24 can be G, A, T or C.

<400> 51

gagcctgcag agctcaggnn nnnn 24

<210> 52

<211> 23

<212> DNA

<213> Artificial sequence

<220>

<223> Synthetic PCR primer used to re-amplify randomply amplified E. co
li genomic DNA sequence.

<220>

<221> misc_feature

<222> (1)..(23)

<223> Synthetic PCR primer used to re-amplify randomly amplified E. col
i genomic DNA sequences.

<400> 52

cgtgcgagcc tgcagagctc agg 23

<210> 53

<211> 45

<212> PRT

<213> Artificial sequence

<220>

<223> Barstar binding barnase-p3 fusion insert.

<220>

<221> MISC_FEATURE

<222> (1)..(45)

<223> Barstar binding barnase-p3 fusion insert

<400> 53

Leu Gln Ser Ser Gly Asp Cys Val Ile Ser Asp Thr Cys Ile Ala Gly
1 5 10 15

Met Ala Glu Ala Ala Ala Cys Glu Glu Lys Phe Ser Ser Gln Asn Val
20 25 30

Gly Leu Thr Ile Thr Val Thr Pro Cys Leu Ser Ser Ala

35 40 45

<210> 54

<211> 44

<212> PRT

<213> Artificial sequence

<220>

<223> Barstar binding barnase-p3 fusion insert.

<220>

<221> MISC_FEATURE

<222> (1)..(44)

<223> Barstar binding barnase-p3 fusion insert

<400> 54

Leu Gln Ser Ser Gly Cys Gly Ser Ser Gly Ser Ser Ile Asn Cys Leu

1 5 10 15

Pro Cys Gly Ala Thr Ser Arg Gly Thr Ser Pro Leu Ala Ser Gly Leu

20 25 30

Pro Ser Ser Ala Thr Ile His Cys Leu Ser Ser Ala

35 40

<210> 55

<211> 40

<212> PRT

<213> Artificial sequence

<220>

<223> Barstar binding barnase-p3 fusion insert.

<220>

<221> MISC_FEATURE

<222> (1)..(40)

<223> Barstar binding barnase-p3 fusion insert

<400> 55

Leu Gln Ser Ser Gly Asp Ser Ala Gly Cys Lys Asn Met Thr Gly Gly

1 5 10 15

Arg Leu Tyr Ala His Thr Leu Glu Ala Ile Ile Pro Gly Phe Ala Val

20 25 30

Ser Ala Pro Ala Cys Glu Pro Ala

35 40

<210> 56

<211> 33

<212> PRT

<213> Artificial sequence

<220>

<223> Barstar binding barnase-p3 fusion insert.

<220>

<221> MISC_FEATURE

<222> (1)..(33)

<223> Barstar binding barnase-p3 fusion insert

<400> 56

Leu Gln Ser Ser Gly Cys Val Arg Leu Lys Arg Thr Ser Val Asn His

1 5 10 15

Gln Pro Asp Ala Trp Pro Glu Pro His Leu Lys Ala Ala Cys Glu Pro

20 25 30

Ala

<210> 57

<211> 44

<212> PRT

<213> Artificial sequence

<220>

<223> Barstar binding barnase-p3 fusion insert.

<220>

<221> MISC_FEATURE

<222> (1)..(44)

<223> Barstar binding barnase-p3 fusion insert

<400> 57

Leu Gln Ser Ser Gly Cys Gly Ser Ser Gly Ser Ser Ile Asn Cys Leu
1 5 10 15

Pro Cys Gly Ala Thr Ser Arg Gly Thr Ser Pro Leu Ala Ser Gly Leu
20 25 30

Pro Ser Ser Ala Thr Val Gln Cys Leu Ser Ser Ala

35 40

<210> 58

<211> 41

<212> PRT

<213> Artificial sequence

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<223> Barstar binding barnase-p3 fusion insert.

<220>

<221> MISC_FEATURE

<222> (1)..(41)

<223> Barstar binding barnase-p3 fusion insert

<400> 58

Leu Gln Ser Ser Gly Lys Ile Val Gln Ala Gly Ala Asn Ile Gln Asp

1 5 10 15

Gly Cys Ile Met His Gly Tyr Cys Asp Thr Asp Thr Ile Val Gly Glu

20 25 30

Asn Gly His Ile Gly Leu Ser Ser Ala

35 40

<210> 59

<211> 45

<212> PRT

<213> Artificial sequence

<220>

<223> Barstar binding barnase-p3 fusion insert.

<220>

<221> MISC_FEATURE

<222> (1)..(45)

<223> Barstar binding barnase-p3 fusion insert

<400> 59

Leu Gln Ser Ser Gly Val Cys Val Ile Ser Asp Thr Cys Ile Ala Gly

1 5 10 15

Thr Ala Glu Ala Ala Ala Cys Glu Glu Lys Phe Ser Ser Gln Asn Val

20 25 30

Gly His Thr Ile Thr Glu Thr Pro Cys Leu Ser Ser Ala

35 40 45

<210> 60

<211> 44

<212> PRT

<213> Artificial sequence

<220>

<223> Barstar binding barnase-p3 fusion insert.

<220>

<221> MISC_FEATURE

<222> (1)..(44)

<223> Barstar binding barnase-p3 fusion insert

<400> 60

Leu Gln Ser Ser Gly Cys Gly Ser Ser Gly Ser Ser Ile Asn Cys Leu

1 5 10 15

Pro Cys Gly Ala Thr Ser Arg Gly Thr Ser Pro Leu Ala Ser Gly Leu

20 25 30

Pro Ser Ser Ala Thr Ile Gln Cys Leu Ser Ser Ala

35 40

<210> 61

<211> 53

<212> PRT

<213> Artificial sequence

<220>

<223> Barstar binding barnase-p3 fusion insert.

<220>

<221> MISC_FEATURE

<222> (1)..(53)

<223> Barstar binding barnase-p3 fusion insert

<400> 61

Leu Gln Ser Ser Gly Gln Asp Ser Gln Arg Glu His Ala Ser His Thr

1 5 10 15

Ala Glu Asp Asp Cys Glu Asp Gln Thr Arg Ile His Gln His Ile Arg

20 25 30

Glu Val Asp Phe Val Asp Thr Pro Gln Glu Val Asp Asp Cys Arg Ala
35 40 45

Ala Leu Ser Ser Ala
50

<210> 62

<211> 33

<212> PRT

<213> Artificial sequence

<220>

<223> Barstar binding barnase-p3 fusion insert.

<220>

<221> MISC_FEATURE

<222> (1)..(33)

<223> Barstar binding barnase-p3 fusion insert

<400> 62

Leu Gln Ser Ser Gly Cys Val Arg Leu Lys Arg Thr Ser Val Asn His
1 5 10 15

Gln Pro Asp Ala Trp Pro Glu Pro His Leu Lys Ala Ala Cys Glu Pro

20 25 30

Ala

<210> 63

<211> 9

<212> PRT

<213> Artificial sequence

<220>

<223> Barstar binding barnase-p3 fusion insert.

<220>

<221> MISC_FEATURE

<222> (1)..(9)

<223> Barstar binding barnase-p3 fusion insert

<400> 63

Leu Gln Ser Ser Gly Val Arg Pro Ala

1 5

<210> 64

<211> 44

<212> PRT

<213> Artificial sequence

<220>

<223> Barstar binding barnase-p3 fusion insert.

<220>

<221> MISC_FEATURE

<222> (1)..(44)

<223> Barstar binding barnase-p3 fusion insert

<400> 64

Leu Gln Ser Ser Gly Cys Gly Ser Ser Gly Ser Ser Ile Asn Cys Leu
1 5 10 15

Pro Cys Gly Ala Thr Ser Arg Gly Thr Ser Pro Leu Ala Ser Gly Leu
20 25 30

Pro Ser Ser Ala Thr Ile Gln Cys Leu Ser Ser Ala
35 40

<210> 65

<211> 30

<212> PRT

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<220>

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<222> (1)..(30)

<223> Barstar binding barnase-p3 fusion insert

<400> 65

Leu Gln Ser Ser Gly Thr Glu Val Asp Arg Gly Asn Gln Gln His Asp
1 5 10 15

Thr Asn Asp Arg Asp Phe Thr His Thr Pro Leu Ser Ser Ala
20 25 30

<210> 66

<211> 36

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<222> (1)..(36)

<223> Barstar binding barnase-p3 fusion insert

<400> 66

Leu Gln Ser Ser Gly Val Ala Gln Gly Ser Ser Ala Ser Val Asp Val
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Thr Ala Thr Asn Ala Val Leu Ser Ala Asp Ser Leu Ser Leu Gly Gly
20 25 30

Gly Glu Pro Ala
35

<210> 67

<211> 19

<212> PRT

<213> Artificial sequence

<220>

<223> Barstar binding barnase-p3 fusion insert.

<220>

<221> MISC_FEATURE

<222> (1)..(19)

<223> Barstar binding barnase-p3 fusion insert

<400> 67

Leu Gln Ser Ser Gly Gly Ala Val Ala Val Thr Pro Gly Pro Val Leu
1 5 10 15

Ser Ser Ala

<210> 68

<211> 18

<212> PRT

<213> Artificial sequence

<220>

<223> Barstar binding barnase-p3 fusion insert.

<220>

<221> MISC_FEATURE

<222> (1)..(18)

<223> Barstar binding barnase-p3 fusion insert

<400> 68

Leu Gln Ser Ser Gly His Cys Arg Gly Lys Pro Val Leu Cys Thr His
1 5 10 15

Thr Ala

<210> 69

<211> 9

<212> PRT

<213> Artificial sequence

<220>

<223> Barstar binding barnase-p3 fusion insert.

<220>

<221> MISC_FEATURE

<222> (1)..(9)

<223> Barstar binding barnase-p3 fusion insert

<400> 69

Leu Gln Ser Ser Gly Val Arg Pro Ala
1 5

<210> 70

<211> 36

<212> PRT

<213> Artificial sequence

<220>

<223> Barstar binding barnase-p3 fusion insert.

<220>

<221> MISC_FEATURE

<222> (1)..(36)

<223> Barstar binding barnase-p3 fusion insert

<400> 70

Leu Gln Ser Ser Gly Glu Pro Ala Pro Ala His Glu Ala Lys Pro Thr
1 5 10 15

Glu Ala Pro Val Ala Lys Ala Glu Ala Lys Pro Glu Thr Pro Ala His
20 25 30

Leu Ser Ser Ala
35

<210> 71

<211> 33

<212> PRT

<213> Artificial sequence

<220>

<223> Barstar binding barnase-p3 fusion insert.

<220>

<221> MISC_FEATURE

<222> (1)..(33)

<223> Barstar binding barnase-p3 fusion insert

<400> 71

Leu Gln Ser Ser Gly Cys Val Arg Leu Lys Arg Thr Ser Val Asn His
1 5 10 15

Gln Pro Asp Ala Trp Pro Glu Pro His Leu Lys Ala Ala Cys Glu Pro

20 25 30

Ala

<210> 72

<211> 36

<212> PRT

<213> Artificial sequence

<220>

<223> Barstar binding barnase-p3 fusion insert.

<220>

<221> MISC_FEATURE

<222> (1)..(36)

<223> Barstar binding barnase-p3 fusion insert

<400> 72

Leu Gln Ser Ser Gly Val Val Asp Trp Ala Lys Met Arg Glu Ile Ala

1 5 10 15

Asp Ser Ile Gly Ala Tyr Leu Phe Val Asp Met Ala His Val Ala Ala

20 25 30

Leu Ser Ser Ala

35

<210> 73

<211> 117

<212> DNA

<213> Artificial sequence

<220>

<223> Vector pK1 polylinker sequence.

<220>

<221> misc_feature

<222> (1)..(117)

<223> Vector pK1 polylinker sequence

<400> 73

aatgctggcg gcggcccagc cggcctttct gaggggtcga ctatagaagg acgaggggcc 60

cacgaaggag gtggggtacc cggttccgag ggtggttccg gttccggtga ttttgat 117

<210> 74

<211> 39

<212> PRT

<213> Artificial sequence

<220>

<223> Polypeptide encoded by pK1 vector polylinker sequence.

<220>

<221> MISC_FEATURE

<222> (1)..(39)

<223> Polypeptide encoded by pK1 vector polylinker sequence

<400> 74

Asn Ala Gly Gly Gly Pro Ala Gly Leu Ser Glu Gly Ser Thr Ile Glu
1 5 10 15

Gly Arg Gly Ala His Glu Gly Gly Gly Val Pro Gly Ser Glu Gly Gly
20 25 30

Ser Gly Ser Gly Asp Phe Asp
35

<210> 75

<211> 117

<212> DNA

<213> Artificial sequence

<220>

<223> Vector pK2 polylinker sequence.

<220>

<221> misc_feature

<222> (1)..(117)

<223> vector pK2 polylinker sequence

<400> 75

aatgctggcg gcggcccagc cggcctttct gaggggtcga ctatagaagg acgagggccc 60

acgaagcagc tggggtaccg gttccgaggg tggttccggt tccggtgatt ttgatta 117

<210> 76

<211> 39

<212> PRT

<213> Artificial sequence

<220>

<223> Polypeptide sequence encoded by vector pK2 polylinker region.

<220>

<221> MISC_FEATURE

<222> (1)..(39)

<223> Polypeptide sequence encoded by vector pK2 polylinker region.

<220>

<221> MISC_FEATURE

<222> (38)..(38)

<223> X represents a TGA stop codon

<220>

<221> MISC_FEATURE

<222> (36)..(36)

<223> X represents a stop codon (TGA)

<400> 76

Asn Ala Gly Gly Gly Pro Ala Gly Leu Ser Glu Gly Ser Thr Ile Glu

1 5 10 15

Gly Arg Gly Pro Thr Lys Gln Leu Gly Tyr Arg Phe Arg Gly Trp Phe

20 25 30

Arg Phe Arg Xaa Phe Xaa Leu
35

<210> 77
<211> 35
<212> DNA
<213> Artificial sequence

<220>
<223> Sequence of the junction region between Barnase and p3 in recombi
nant fusion vector fd-3.

<220>
<221> misc_feature
<222> (1)..(35)
<223> Sequence of the junction region between Barnase and p3 in recombi
nant fusion vector fd-3.

<400> 77
atcagactgc aggcggtgcg gccgcagaaa ctgtt 35

<210> 78
<211> 11
<212> PRT

<213> Artificial sequence

<220>

<223> Amino acid sequence about the junction of Barnase and p3 coding r
egions of recombinant fusion vector fd-3.

<400> 78

Ile Arg Leu Gln Ala Ala Ala Ala Glu Thr Val
1 5 10

<210> 79

<211> 4

<212> PRT

<213> Artificial sequence

<220>

<223> Factor Xa protease cleavage sequence.

<220>

<221> MISC_FEATURE

<222> (1)..(1)

<223> X can be either Ile or Leu.

<220>

<221> MISC_FEATURE

<222> (1)..(4)

<223> Factor Xa proteolytic cleavage site.

<400> 79

Xaa Glu Gly Arg

1

??

??

(continued...)

(continued...)

Serial No. 09/710,444 File No. 8039/1090 By: (MBW) KMW

Applicant(s): Riechmann, et al.

Title: Selection System

The Following, DUE _____ in the USPTO, was received by the PTO Mail Room on the date stamped hereon:

[ ] Cert. of Mailing by Express Mail (37 CFR 1.10)
Express Mail Label No. _____
[—] Cert. of Mailing under 37 CFR 1.8(a)
[ ] Patent Application (_____ total pgs)
[ ] Provisional or [ ] Non-Provisional
(pgs) Specification (pgs) Abstract,
(pgs) Claims (_____# claims)
[ ] New Patent Application Transmittal
[ ] Provisional Patent Application Cover Sheet
[ ] Declaration and Power of Attorney
[ ] Application Data Sheet
[ ] Drawings _____ Sheet(s) (FIGS. _____ - _____)
[ ] Formal or [ ] Informal
[ ] Assignment of _____
[ ] Recordation Cover Sheet Form PTO-1595
[ ] Information Disclosure Statement
[ ] Form PTO 1449 and Copies of Cited References

[ ] Response to Notice to File Missing Parts
[ ] Copy of Part 2 of NFMP
[—] Diskette Containing Nucleotide and/or Amino Acid Sequence Listing Substitute
[ ] Priority Document(s) # _____
[—] Amendment/Response
[ ] Petition for Extension of Time (x2)
[ ] Check in the amount of _____
Check # _____
[ ] Transmittal of Formal Drawings
[ ] Motion/Opposition/Reply
[ ] Request for Cont'd Examination (RCE)
[ ] Notice of Appeal
[ ] Appeal Brief (x3)
[ ] Issue Fee Transmittal
[—] Transmittal Letter (x2)

[—] Other Substitute Paper Copy of the Sequence Listing", Copy of Notice to Comply", Statement Under 37 CFR 1.821(f) + (6)

MAILED April 8, 2003

Atty. Docket No.: 8039/1090 **PATENT**

IN THE UNITED STATES PATENT AND TRADEMARK OFFICE

Application of:	Riechmann, et al.	Examiner:	B. Celsa
Serial No.:	09/710,444		
Filed:	November 10, 2000	Group Art Unit:	1627
Entitled:	"Selection System"		
		Conf. No.:	2736

CERTIFICATE OF MAILING UNDER 37 C.F.R. § 1.8a

I hereby certify that this correspondence (and any paper or fee referred to as being enclosed) is being deposited with the United States Post Office as First Class Mail on the date indicated below in an envelope addressed to: U.S. Patent & Trademark Office, Box: Sequence, P.O. Box 2327, Arlington, VA 22202.

Mary Wilson
Name of Person Mailing Paper

Signature of Person Mailing Paper

U.S. Patent and Trademark Office
Box: Sequence
P.O. Box 2327
Arlington, VA 22202

TRANSMITTAL LETTER

Enclosed for filing the above-identified patent application, please find the following documents:

1. Amendment in Response to Notice to Comply dated February 27, 2002;
2. Copy of Notice to Comply;
3. Paper Copy of the Sequence Listing (59 pgs);
4. Computer Readable Copy of the Sequence Listing;
5. Sequence Statement Under 37 C.F.R. § 1.821(f) and (g);
6. Petition for Four Month's Extension of Time;
7. Check in the amount of $720.00; and
8. Return Post Card.

The Commissioner for Patents is hereby authorized to charge any additional fees or credit any overpayment in the total fees to Deposit Account No. 16-0085, Reference 8039/1090. A duplicate of this transmittal letter is enclosed for this purpose.

Respectfully submitted,

Mark J. Fitzgerald
Reg. No. 45,928 for
Kathleen Williams

Date: July 25, 2002

Docket #
Response due
Statutory period
Palmer & Dodge LLP
Patent Department

Name: Kathleen Williams
Registration No.: 34,380
Customer No.: 29933
Palmer & Dodge LLP
111 Huntington Avenue
Boston, MA 02199-7613 Tel: 617-239-0100

Atty. Docket No.: 8039/1090 **PATENT**

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Kathleen Williams

Date: July 25, 2002

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Palmer & Dodge LLP
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Mary Wilson
Name of Person Mailing Paper

Mary M
Signature of Person Mailing Paper

U.S. Patent and Trademark Office
Box: Sequence
P.O. Box 2327
Arlington, VA 22202

PETITION FOR EXTENSION OF TIME

Dear Sir:

Applicant respectfully petitions under 37 C.F.R. § 1.136(a) for an Extension of Time of four months to file a Response in the above-identified patent application. This will serve to extend the time for filing the Response to the Notice to Comply mailed February 27, 2002 from March 27, 2002, up to and including July 27, 2002.

Pursuant to 37 C.F.R. § 1.17, enclosed is the requisite extension fee of $720.00 for maintaining the pendency of the present application. The Commissioner of Patents is hereby authorized to charge any additional fees or credit any overpayment to Deposit Account No. 16-0085, Reference No. 8039/1090. A duplicate of this letter is enclosed for that purpose.

Respectfully submitted, Mark J. FitzGerald Reg. No. 45,928 for Kathleen M. Williams

Date: July 25, 2002

Name: Kathleen Williams
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Tel: 617-239-0100

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Application of:	Riechmann, et al.	Examiner:	B. Celsa
Serial No.:	09/710,444		
Filed:	November 10, 2000	Group Art Unit:	1627
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		Conf. No.:	2736

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Name of Person Mailing Paper

Mary W
Signature of Person Mailing Paper

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Respectfully submitted, Mark J. FitzGerald
Reg. No. 45,928 for
Kathleen M. Williams

Date: July 25, 2002

Name: Kathleen Williams
Registration No.: 34,380
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Name of Person Mailing Paper

Signature of Person Mailing Paper

U.S. Patent and Trademark Office
Box: Sequence
P.O. Box 2327
Arlington, VA 22202

STATEMENT UNDER 37 C.F.R. §1.821 (f) and (g)

Sir:

This paper is submitted in response to the Notice to Comply mailed by the USPTO on February 27, 2002.

In accordance with 37 C.F.R. §1.821 (f) I hereby state that the paper copy and the computer readable form of the Sequence Listing submitted herewith in the above-identified patent application are supported in the application and contain no new matter. I hereby state that the information recorded in computer readable form is identical to the written sequence listing.

In accordance with 37 C.F.R. §1.821 (g), I hereby state that the computer readable form of the Sequence Listing submitted herewith contains no new matter.

Mark J. FitzGerald
Reg. No. 45,928 for
Kathleen Williams

7/25/02
Date

Kathleen Williams
Reg. No. 34,380
Attorney for Applicant
Palmer & Dodge LLP
111 Huntington Avenue
Boston, MA 02199-7613
Tel: (617) 239-0451
Fax: (617) 227-4420

Atty. Docket No.: 8039/1090 PATENT

IN THE UNITED STATES PATENT AND TRADEMARK OFFICE

Application of:	Riechmann, et al.	Examiner:	B. Celsa
Serial No.:	09/710,444		
Filed:	November 10, 2000	Group Art Unit:	1627
Entitled:	"Selection System"		
		Conf. No.:	2736

CERTIFICATE OF MAILING UNDER 37 C.F.R. § 1.8a

I hereby certify that this correspondence (and any paper or fee referred to as being enclosed) is being deposited with the United States Post Office as First Class Mail on the date indicated below in an envelope addressed to: U.S. Patent & Trademark Office, Box: Sequence, P.O. Box 2327, Arlington, VA 22202.

Mary Wilson
Name of Person Mailing Paper

Signature of Person Mailing Paper

U.S. Patent and Trademark Office
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Arlington, VA 22202

AMENDMENT

Sir:

This is filed in response to the Examiner's Notice to Comply with nucleotide or amino acid sequence listing requirements mailed February 27, 2002 in the above noted U.S. Patent Application. Kindly enter the following amendments and remarks.

In the Specification:

Replace the paragraph at lines 14 to 23 on page 15 with the following replacement paragraph:

A sequence (PAGLSEGSTIEGRGAHE; SEQ ID NO: 1) comprising several proteolytic sites is inserted in the flexible glycine-rich region between the D2 and D3 domains of the phage p3. Incubation of the phage (fd-K108) under native conditions with trypsin, thermolysin or subtilisin now resulted in almost complete loss of infectivity (from 10^7 to < 10 TU/ml) and incubation with Glu-C and chymotrypsin resulted in a major loss (from 10^7 to 10^4 TU/ml). This indicates that these proteases cleave the new linker. However incubation with Factor Xa, Arg-C or thrombin did not lead to a loss in infectivity, despite the presence of potential cleavage sites

for these enzymes. Presumably the presence of the D2 and D3 domains may block access or cleavage for these enzymes in the case of the present polypeptide.

Replace Table 4, on page 24, with the following replacement Table 4:

Table 4. Primer sequences

pklinker	5'GGCACCCTCAGAACGGTACCCCACCCTCAGAGGCCGGCTGGG CCGCCACCCTCAGAG 3' (SEQ ID NO: 2)
polyXafor	5'GGTGGCGGCCCAGCCGGCCTTTCTGAGGGGTCGACTATAGAA GGACGAGGGCCCAGCGAAGGAGGTGGGGTACCCCCTTCTGAGG GTGG 3' (SEQ ID NO: 3)
polyXaback	5'CCACCCTCAGAAGGGGGTACCCCACCTCCTTCGCTGGGCCCT CGTCCTTCTATAGTCGACCCCTCAGAAAGGCCGGCTGGGCCGC CACC 3' (SEQ ID NO: 4)
fdPCRBack	5'GCGATGGTTGTTGTCATTGTCGGC 3' (SEQ ID NO: 5)
LIBSEQfor	5'AAAAGAAACGCAAAGACACCACGG 3' SEQ ID NO: 6)
LIBSEQback	5'CCTCCTGAGTACGGTGATACACC 3' (SEQ ID NO: 7)
LSPAf or	5'GTAAATTCAGAGACTGCGCTTTCC 3' (SEQ ID NO: 8)
LSPAback	5'ATTTTCGGTCATAGCCCCCTTATTAG 3' (SEQ ID NO: 9)
Flagprimer	5'CAACGGGCGGCCGCAGACTACAAGGATGACGACGACAAGG AAACTGTTGAAAGTTGTTTAGCAA 3' (SEQ ID NO: 10)
RECGLYfor	5'CCCCTCAGAAAGGCCGGCTGGGCCGCCGCCAGCATTGACAG GAGGTTCAGG 3' (SEQ ID NO: 11)
RECGLYback	5'GAAGGAGGTGGGGTACCCGGTTCCGAGGGTGGTTCCGGTTC CGGTGATTTTG 3' (SEQ ID NO: 12)
delcKpn	5'CCCTCGGAACCGGTACCCCAGCTGCTTCGTGGGCCC 3' (SEQ ID NO: 13)
Barnasefor	5'CTGGCGGCGGCCCAGCCGGCCCTGCACAGGTTATCAACACG TTTGAC 3' (SEQ ID NO: 14)
BarnaseH102Aba ck	5'CTCGGAACCGGTACCTCTGATTTTTGTAAAGGTCTGATAAGC G 3' (SEQ ID NO: 15)
villinfor	5'GGCGGCCCAGCCGGCCTTTCTCTCTCTGACGAGGACTTCAAG GC 3' (SEQ ID NO: 16)
villinback	5'CCTCGGAACCGGTACCGAAGAGTCCTTTCTCCTTCTTGAGG 3' (SEQ ID NO: 17)

-Replace the paragraph at page 30, lines 4-14 with the following replacement paragraph:

--1: TACGCCAAGCTTGCATGC (SEQ ID NO: 18);

2: CTGCACCTGGGCCATGG (SEQ ID NO: 19);

3: GATTACGCCAAGCTTTG (SEQ ID NO: 20);

4: GATTACGCC*AAGCTT*GCATGCANNDDCTNTDTCAAGGAGACAGTCATAATGARRN NBCTATTGSYAAYRSYASYASYAGBNTTGTTATTACTCSYANYCVNNCYGD*CCATGG* CCCAGGTGCAGCTG (SEQ ID NO: 21);

5: GATTACGCC*AAGCTT*TGNNNNCTTTTTTWWGGAGATTTCAACRTGARAARATTAT TATTCSYAATTSYTTTAGTTSYTSYTTTCTWTGYGGYCCAGCCGG*CCATGG*CCCAGGT GCA. (SEQ ID NO: 22)

6: CTTTATGCTTCCGGCTCG. (SEQ ID NO: 23)

7: CGGCCCCATTCAGATCC. (SEQ ID NO: 24)--

Replace Table 7, on pages 35 and 36, with the following replacement Table 7. Because portions of the original text are underlined, the present amendments are indicated by double underlines.

Table 7. Randomised and selected sequences.

The randomised DNA sequence is given from 5' to 3'; above and below it, the bases that differ from the given sequence in the signal sequences pe1B, 17, 19, 110 and 112 are indicated. The Shine-Delgarno sequence, the start codon and the last codon of the signal sequence, GCC, have been underlined. The HindIII and the NcoI restriction sites are in italics. The corresponding amino acid sequences are given below. Library I is initially designed from the pelB leader and library II from the g3 leader.

III-A. From library I

pelB (SEQ ID NO: 25) AATT A T AATAC

5' *AAGCTT*GCATGCANNDDCTNT DTCAAGGAGACAGTCATAAATGARRNNB CT (SEQ ID NO:26)

17 (SEQ ID NO: 27) GCAT C G AGACG
110 (SEQ ID NO: 28) CGGG G T GAGGG
112 (SEQ ID NO: 29) CCAG C T GGCGG

pelB CCT CGGC GCCGCT GA GCGGC CAG C G (SEQ ID NO: 30)

ATTGSYAAYRSYASYASYAGBNTTGTTATTACTC SYANY CVNNCYGD*CCATGG* CC 3' (SEQ ID NO: 31)

17 GC TGGT CT GT GA CC CC GGT C T (SEQ ID NO: 32)

110 GC TGCT GT GC GG CC AT GCG C G (SEQ ID NO: 33)

112 GT TAGC CG CT GG CT GC CCC C A (SEQ ID NO: 34)

pelB M K Y L L P T A A A G L L L L A A Q P A M A (SEQ ID NO: 35)

17 K T A M V L V G P P G P S (SEQ ID NO: 36)

110 R G A M L V A G P I A P A (SEQ ID NO: 37)

112 R R V I A A V G L A P P T (SEQ ID NO: 38)

III-B. From library II

g3leader GAGC TT G A A (SEQ ID NO: 39)

5' *AAGTT*GNNNNCTTTTTTWWGGAGATTTTCAACRTGARAARATTATTAT (SEQ ID NO: 40)

19 GGGC TA A G G (SEQ ID NO: 41)

GC CC GT CC A C C (SEQ ID NO: 42)

TCSYAATTSYTTTAGTTSYTSYTTTCTWTGYGGYCCAGCCGG*CCATGG* CC3' (SEQ ID NO: 43)

19 CT CC GT GC A T T (SEQ ID NO: 44)

g3 leader M K K L L F A I P L V V P F Y A A Q P A M A (SEQ ID NO: 45)

19 R R L P V A Y V V (SEQ ID NO: 46)

Replace the paragraph at lines 8-17 on page 38 with the following replacement paragraph:

The phage displaying the Stoffel fragment are incubated with primer **13** [TTT CGC AAG ATG TGG CGT] (SEQ ID NO: 47) comprising a 5' maleimidyl group and a 3' biotinylated nucleotide. After incubation the phage are captured on streptavidin-coated beads, with a yield of about 1-5% of infectious phage. This shows that primer can be chemically cross-linked to the phage, presumably via p8 protein as shown for the N-biotinoyl-N'(6-maleimidohexanoyl) bydrazide. The phage are then incubated with primer **1b** [GCGAAGATGTGG] (SEQ ID NO: 48) comprising a 5' maleimidyl group in the presence of biotin-dUTP **2** and template **3** [AAA TAC AAC AAT AAA ACG CCA CAT CTT GCG] (SEQ ID NO: 49). Capture of the phage is dependent on presence of **1b**, **2** and **3** (Table 8), but also on the inclusion of trypsin, which cleaves the helper phage to reduce non-specific phage isolation.

Replace the paragraph at page 39, lines 19-27 with the following replacement paragraph:

For the cloning of (poly)-peptide encoding DNA fragments and their display for selection between barnase and p3, the phage fd-3 is constructed (Fig. 5). Phage fd-3 comprises the H1021A mutant of barnase N-terminally fused to the p3 gene of phage fd.TET. Between the codon for the last residue of barnase and the first residue of p3 is the nucleotide sequence *CTG GAG* GCG GTG CGG CCG CA (SEQ ID NO: 50). This sequence contains a PstI DNA restriction site (in italics) for insertion of DNA fragments flanked by PstI restriction sites. The sequence further introduces a frame shift between barnase and p3, which prevents expression of the correct p3 reading frame in fd-3. Phage particles of phage fd-3 therefore do not display the infection protein p3 and are non-infectious.

Replace the paragraph at page 40, lines 8-23 with the following replacement paragraph:

Genomic DNA from the *E. coli* strain TG1 is amplified in 30 cycles of a polymerase chain reaction (PCR) with an annealing temperature of 48°C using the oligonucleotide SN6MIX (5'-GAG *CCT GCA* **GAG CTC** AGG NNN NNN-3'; SEQ ID NO: 51), which comprises 6 degenerate positions at the extendible 3' end to ensure random priming. In a second step of 30 PCR cycles with an annealing temperature of 52°C primary PCR products are extended by re-amplification with the oligonucleotide XTND (5'-CGT GCG AGC *CTG CAG* **AGC TCA** GG-3'; SEQ ID NO: 52). Products with a length of around 150 bp from this reaction are purified from an agarose gel and reamplified in 30 PCR cycles using an annealing temperature of 52°C and the oligonucleotide XTND. These reamplified 150 bp fragments are partially digested with SacI (site indicated in bold in the oligonucleotides) and ligated for dimerisation. Ligated products are reamplified in a further 10 PCR cycles with an annealing temperature of 44°C followed by a 30 PCR cycles with an annealing temperature of 55°C using the oligonucleotide XTND. The annealing temperatures are chosen to discriminate against priming of the oligonucleotide in the middle of the dimerised fragments. The reaction product is size purified twice on an agarose gel to remove monomers and oligomers (non-dimers).

Replace the table on page 44 (Table 9) with the following replacement table:

Phage clone	Proteolytic selection	Barstarbindg -DTT	+DTT	Amino acid sequence of inserts
TA-1.2	1xTr	yes	no	LQSSGDCVIS DTCIAGMAEA AACEEKFSSQ NVGLTITVTP CLSSA (SEQ ID NO: 53)
TA-2.25	2xTr	yes	no	LQSSGCGSSG SSINCLPCGA TSRGTSPLAS GLPSSATIHC LSSA (SEQ ID NO: 54)
TA-2.26	2xTr	yes	no	LQSSGDSAGC KNMTGGRLYA HTLEAIIPGF AVSAPACEPA (SEQ ID NO: 55)
TA-2.27	2xTr	yes	yes	LQSSGCVRLK RTSVNHQPDA WPEPHLKAAC EPA (SEQ ID NO: 56)
TA-2.30	2xTr	yes	no	LQSSGCGSSG SSINCLPCGA TSRGTSPLAS GLPSSATVQC LSSA (SEQ ID NO: 57)
TB-1.10	1xTh	yes	yes	LQSSGKIVQA GANIQDGCIM HGYCDTDTIV GENGHIGLSS A (SEQ ID NO: 58)
TB-1.11	1xTh	yes	yes	no insert, Barnase & p3 in frame
TB-2.33	2xTh	yes	no	LQSSGVCVIS DTCIAGTAEA AACEEKFSSQ NVGHTITETP CLSSA (SEQ ID NO: 59)
TB-2.34	2xTh	yes	no	LQSSGCGSSG SSINCLPCGA TSRGTSPLAS GLPSSATIQC LSSA (SEQ ID NO: 60)
TE-2.35	2xTh	yes	no	LQSSGQDSQR EHASHTAEDD CEDQTRIHQH IREVDFVDTP QEVDDCRAAL SSA (SEQ ID NO: 61)
TB-2.37	2xTh	yes	no	LQSSGCVRLK RTSVNHQPDA WPEPHLKAAC EPA (SEQ ID NO: 62)
TB-2.38	2xTh	yes	yes	LQSSGVRPA (SEQ ID NO: 63)
TB-2.39	2xTh	yes	no	LQSSGCGSS GSSINCLPCGA TSRGTSPLAS GLPSSATIQ CLSSA (SEQ ID NO: 64)

Replace the table at lines 12-29 on page 46 with the following replacement table:

Phage clone	Proteolytic selection	Barstarbindg +DTT	Amino acid sequence of inserts
B2-13 (SEQ ID NO: 65)	2xTr/Th	yes	LQSSGTEVDR GNQQHDTNDR DFTHTPLSS A
B2-14	2xTr/Th	yes	LQSSG5VAQG SSASVDVTAT NAVLSADSL SLGGGEPA (SEQ ID NO: 66)
B2-22	2xTr/Th	yes	LQSSGGAVAV TPGPVLSSA (SEQ ID NO: 67)
B2-23	2xTr/Th	yes	LQSSGHCRGK PVLCTHTA (SEQ ID NO: 68)
B2-15	2xTr/Th	yes	LQSSGVRPA (SEQ ID NO: 69)
B2-17	2xTr/Th	yes	no insert, Barnase & p3 in frame
B2-20,21	2xTr/Th	yes	no insert, Barnase & p3 in frame
B2-16,24	2xTr/Th	yes	LQSSGEPAPA HEAKPTEAPV AKAEAKPETP AHLSSA (SEQ ID NO: 70)
B2-18	2xTr/Th	no	LQSSGCVRLK RTSVNHQPDA WPEPHLKAAC EPA (SEQ ID NO: 71)
B2-19	2xTr/Th	no	LQSSGVVDWA KMREIADSIG AYLFVDMAHV AALSSA (SEQ ID NO: 72)

Replace the paragraph at page 47, lines 8-10 with the following replacement paragraph:

Figure 2. The phagemid vectors pK1 and pK2. These vectors contain a protease cleavable sequence between D2 and D3 of the phage p3 protein. In pK1, D2 + D3 are in frame; in pK2, D3 is out of frame. Nucleotide and amino acid sequence for the polylinker regions are shown for pK1 (SEQ ID NO: 73 and SEQ ID NO: 74, respectively) and pK2 (SEQ ID NO: 75 and SEQ ID NO: 76, respectively).

Replace the paragraph at page 47, lines 21-23 with the following replacement paragraph:

Figure 5. The fd vector fd-3. The gene for the H102A mutant of Barnase is introduced by subcloning into fd-DOG [43] after PCR amplification with suitable oligonucleotides using the restriction sites ApaLI (at the Barnase 5' end) and NotI to create fd-3. The nucleotide and amino

acid sequence of the junction between Barnase and p3 sequences is shown in expanded view (SEQ ID NO 77 and SEQ ID NO: 78, respectively)

REMARKS

The amendments directed herein are made in order to add SEQ ID NOs corresponding to the SEQ ID NOs in the accompanying Sequence Listing. The amendments add no new matter.

Respectfully submitted: Mark J. FitzGerald Reg. No. 45,928 for Kathleen M. Williams

7/25/02
Date

Kathleen M. Williams
Reg. No. 34, 380
Attorney for Applicant
Palmer & Dodge LLP
111 Huntington Avenue
Boston, MA 02199-7613
Tel: (617) 239-0451
Fax: (617) 227-4420

Version of amendments marked to show changes:

- Replace the paragraph at lines 14 to 23 on page 15 with the following replacement paragraph:

-- A sequence (PAGLSEGSTIEGRGAHE; SEQ ID NO: 1) comprising several proteolytic sites is inserted in the flexible glycine-rich region between the D2 and D3 domains of the phage p3. Incubation of the phage (fd-K108) under native conditions with trypsin, thermolysin or subtilisin now resulted in almost complete loss of infectivity (from 10^7 to < 10 TU/ml) and incubation with Glu-C and chymotrypsin resulted in a major loss (from 10^7 to 10^4 TU/ml). This indicates that these proteases cleave the new linker. However incubation with Factor Xa, Arg-C or thrombin did not lead to a loss in infectivity, despite the presence of potential cleavage sites for these enzymes. Presumably the presence of the D2 and D3 domains may block access or cleavage for these enzymes in the case of the present polypeptide.--

- Replace Table 4, on page 24, with the following replacement Table 4:

--Table 4

Table 4. Primer sequences

pklinker	5'GGCACCCTCAGAACGGTACCCCACCCTCAGAGGCCGGCTGGG CCGCCACCCTCAGAG 3' (SEQ ID NO: 2)
polyXafor	5'GGTGGCGGCCCAGCCGGCCTTTCTGAGGGGTCGACTATAGAA GGACGAGGGCCCAGCGAAGGAGGTGGGGTACCCCCTTCTGAGG GTGG 3' (SEQ ID NO: 3)
polyXaback	5'CCACCCTCAGAAGGGGGTACCCCACCTCCTTCGCTGGGCCCT CGTCCTTCTATAGTCGACCCCTCAGAAAGGCCGGCTGGGCCGC CACC 3' (SEQ ID NO: 4)
fdPCRBack	5'GCGATGGTTGTTGTCATTGTCGGC 3' (SEQ ID NO: 5)
LIBSEQfor	5'AAAAGAAACGCAAAGACACCACGG 3' (SEQ ID NO: 6)
LIBSEQback	5'CCTCCTGAGTACGGTGATACACC 3' (SEQ ID NO: 7)
LSPAf or	5'GTAAATTCAGAGACTGCGCTTTCC 3' (SEQ ID NO: 8)
LSPAback	5'ATTTTCGGTCATAGCCCCCTTATTAG 3' (SEQ ID NO: 9)
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RECGLYfor	5'CCCCTCAGAAAGGCCGGCTGGGCCGCCGCCAGCATTGACAG GAGGTTCAGG 3' (SEQ ID NO: 11)
RECGLYback	5'GAAGGAGGTGGGGTACCCGGTTCCGAGGGTGGTTCCGGTTC CGGTGATTTTG 3' (SEQ ID NO: 12)
delcKpn	5'CCCTCGGAACCGGTACCCCAGCTGCTTCGTGGGCCC 3' (SEQ ID NO: 13)
Barnasefor	5'CTGGCGGCGGCCCAGCCGGCCCTGCACAGGTTATCAACACG TTTGAC 3' (SEQ ID NO: 14)
BarnaseH102Aback	5'CTCGGAACCGGTACCTCTGATTTTTGTAAAGGTCTGATAAGC G 3' (SEQ ID NO: 15)
villinfor	5'GGCGGCCCAGCCGGCCTTTCTCTCTCTGACGAGGACTTCAAG GC 3' (SEQ ID NO: 16)
villinback	5'CCTCGGAACCGGTACCGAAGAGTCCTTTCTCCTTCTTGAGG 3' (SEQ ID NO: 17) --

-Replace the paragraph at page 30, lines 4-14 with the following replacement paragraph:

--1: TACGCCAAGCTTGCATGC (SEQ ID NO: 18);

2: CTGCACCTGGGCCATGG (SEQ ID NO: 19);

3: GATTACGCCAAGCTTTG (SEQ ID NO: 20);

4: GATTACGCC*AAGCTT*GCATGCANNDDCTNTDTCAAGGAGACAGTCATAATGARRN NBCTATTGSYAAYRSYASYASYAGBNTTGTTATTACTCSYANYCVNNCYGD*CCATGG* CCCAGGTGCAGCTG (SEQ ID NO: 21);

5: GATTACGCC*AAGCTT*TGNNNNCTTTTTTWWGGAGATTTCAACRTGARAARATTAT TATTCSYAATTSYTTTAGTTSYTSYTTTCTWTGYGGYCCAGCCGG*CCATGG*CCCAGGT GCA. (SEQ ID NO: 22)

6: CTTTATGCTTCCGGCTCG. (SEQ ID NO: 23)

7: CGGCCCCATTCAGATCC. (SEQ ID NO: 24)--

- Replace Table 7, on pages 35 and 36, with the following replacement Table 7. Because portions of the original text are underlined, the present amendments are indicated by double underlining.

--Table 7. Randomised and selected sequences.

The randomised DNA sequence is given from 5' to 3'; above and below it, the bases that differ from the given sequence in the signal sequences pelB, 17, 19, 110 and 112 are indicated. The Shine-Delgarno sequence, the start codon and the last codon of the signal sequence, GCC, have been underlined. The HindIII and the NcoI restriction sites are in italics. The corresponding amino acid sequences are given below. Library I is initially designed from the pelB leader and library II from the g3 leader.

III-A. From library I

pelB (SEQ ID NO: 25) AATT A T AATAC

5' *AAGCTT*GCATGCANNDDCTNT DTCAAGGAGACAGTCATAAATGARRNNB CT (SEQ ID NO:26)

17 (SEQ ID NO: 27) GCAT C G AGACG

110 (SEQ ID NO: 28) CGGG G T GAGGG

112 (SEQ ID NO: 29) CCAG C T GGCGG

pelB CCT CGGC GCCGCT GA GCGGC CAG C G (SEQ ID NO: 30)

ATTGSYAAYRSYASYASYAGBNTTGTTATTACTC SYANY CVNNCYGD*CCATGG* CC 3' (SEQ ID NO: 31)

17 GC TGGT CT GT GA CC CC GGT C T (SEQ ID NO: 32)

110 GC TGCT GT GC GG CC AT GCG C G (SEQ ID NO: 33)

112 GT TAGC CG CT GG CT GC CCC C A (SEQ ID NO: 34)

pelB M K Y L L P T A A A G L L L L A A Q P A M A (SEQ ID NO: 35)

17 K T A M V L V G P P G P S (SEQ ID NO: 36)

110 R G A M L V A G P I A P A (SEQ ID NO: 37)

112 R R V I A A V G L A P P T (SEQ ID NO: 38)

III-B. From library II

g3leader GAGC TT G A A (SEQ ID NO: 39)

5' *AAGTT*GNNNNCTTTTTTWWGGAGATTTTCAACRTGARAARATTATTAT (SEQ ID NO: 40)

19 GGGC TA A G G (SEQ ID NO: 41)

GC CC GT CC A C C (SEQ ID NO: 42)

TCSYAATTSYTTTAGTTSYTSYTTTCTWTGYGGYCCAGCCGG*CCATGG* CC3' (SEQ ID NO: 43)

19 CT CC GT GC A T T (SEQ ID NO: 44)

g3 leader M K K L L F A I P L V V P F Y A A Q P A M A (SEQ ID NO: 45)

19 R R L P V A Y V V (SEQ ID NO: 46)

--Replace the paragraph at lines 8-17 on page 38 with the following replacement paragraph. Please note that the sequences were presented in brackets in the original filed application. The brackets are replaced by parenthesis herein.

--The phage displaying the Stoffel fragment are incubated with primer **13** (TTT CGC AAG ATG TGG CGT) (SEQ ID NO: 47) comprising a 5' maleimidyl group and a 3' biotinylated nucleotide. After incubation the phage are captured on streptavidin-coated beads, with a yield of about 1-5% of infectious phage. This shows that primer can be chemically cross-linked to the phage, presumably via p8 protein as shown for the N-biotinoyl-N'(6-maleimidohexanoyl) bydrazide. The phage are then incubated with primer **1b** (GCGAAGATGTGG) (SEQ ID NO: 48) comprising a 5' maleimidyl group in the presence of biotin-dUTP **2** and template **3** (AAA TAC AAC AAT AAA ACG CCA CAT CTT GCG) (SEQ ID NO: 49). Capture of the phage is dependent on presence of **1b**, **2** and **3** (Table 8), but also on the inclusion of trypsin, which cleaves the helper phage to reduce non-specific phage isolation.--

- Replace the paragraph at page 39, lines 19-27 with the following replacement paragraph:

--For the cloning of (poly)-peptide encoding DNA fragments and their display for selection between barnase and p3, the phage fd-3 is constructed (Fig. 5). Phage fd-3 comprises the H1021A mutant of barnase N-terminally fused to the p3 gene of phage fd.TET. Between the codon for the last residue of barnase and the first residue of p3 is the nucleotide sequence *CTG GAG* GCG GTG CGG CCG CA (SEQ ID NO: 50). This sequence contains a PstI DNA restriction site (in italics) for insertion of DNA fragments flanked by PstI restriction sites. The sequence further introduces a frame shift between barnase and p3, which prevents expression of the correct p3 reading frame in fd-3. Phage particles of phage fd-3 therefore do not display the infection protein p3 and are non-infectious.--

- Replace the paragraph at page 40, lines 8-23 with the following replacement paragraph:

--Genomic DNA from the *E. coli* strain TG1 is amplified in 30 cycles of a polymerase chain reaction (PCR) with an annealing temperature of 48°C using the oligonucleotide SN6MIX (5'-GAG *CCT GCA* **GAG CTC** AGG NNN NNN-3'; SEQ ID NO: 51), which comprises 6 degenerate positions at the extendible 3' end to ensure random priming. In a second step of 30 PCR cycles with an annealing temperature of 52°C primary PCR products are extended by re-amplification with the oligonucleotide XTND (5'-CGT GCG AGC *CTG CAG* **AGC TCA** GG-3'; SEQ ID NO: 52). Products with a length of around 150 bp from this reaction are purified from an agarose gel and reamplified in 30 PCR cycles using an annealing temperature of 52°C and the oligonucleotide XTND. These reamplified 150 bp fragments are partially digested with SacI (site indicated in bold in the oligonucleotides) and ligated for dimerisation. Ligated products are reamplified in a further 10 PCR cycles with an annealing temperature of 44°C followed by a 30 PCR cycles with an annealing temperature of 55°C using the oligonucleotide XTND. The annealing temperatures are chosen to discriminate against priming of the oligonucleotide in the middle of the dimerised fragments. The reaction product is size purified twice on an agarose gel to remove monomers and oligomers (non-dimers).--

- Replace the table on page 44 (Table 9) with the following replacement table:

--Phage clone	Proteolytic selection	Barstarbindg -DTT	+DTT	Amino acid sequence of inserts
TA-1.2	1xTr	yes	no	LQSSGDCVIS DTCIAGMAEA AACEEKFSSQ NVGLTITVTP CLSSA (SEQ ID NO: 53)
TA-2.25	2xTr	yes	no	LQSSGCGSSG SSINCLPCGA TSRGTSPLAS GLPSSATIHC LSSA (SEQ ID NO: 54)
TA-2.26	2xTr	yes	no	LQSSGDSAGC KNMTGGRLYA HTLEAIIPGF AVSAPACEPA (SEQ ID NO: 55)
TA-2.27	2xTr	yes	yes	LQSSGCVRLK RTSVNHQPDA WPEPHLKAAC EPA (SEQ ID NO: 56)
TA-2.30	2xTr	yes	no	LQSSGCGSSG SSINCLPCGA TSRGTSPLAS GLPSSATVQC LSSA (SEQ ID NO: 57)
TB-1.10	1xTh	yes	yes	LQSSGKIVQA GANIQDGCIM HGYCDTDTIV GENGHIGLSS A (SEQ ID NO: 58)
TB-1.11	1xTh	yes	yes	no insert, Barnase & p3 in frame
TB-2.33	2xTh	yes	no	LQSSGVCVIS DTCIAGTAEA AACEEKFSSQ NVGHTITETP CLSSA (SEQ ID NO: 59)
TB-2.34	2xTh	yes	no	LQSSGCGSSG SSINCLPCGA TSRGTSPLAS GLPSSATIQC LSSA (SEQ ID NO: 60)
TE-2.35	2xTh	yes	no	LQSSGQDSQR EHASHTAEDD CEDQTRIHQH IREVDFVDTP QEVDDCRAAL SSA (SEQ ID NO: 61)
TB-2.37	2xTh	yes	no	LQSSGCVRLK RTSVNHQPDA WPEPHLKAAC EPA (SEQ ID NO: 62)
TB-2.38	2xTh	yes	yes	LQSSGVRPA (SEQ ID NO: 63)
TB-2.39	2xTh	yes	no	LQSSGCGSS GSSINCLPCGA TSRGTSPLAS GLPSSATIQ CLSSA (SEQ ID NO: 64) --

- Replace the table at lines 12-29 on page 46 with the following replacement table:

Phage clone	Proteolytic selection	Barstarbindg +DTT	Amino acid sequence of inserts
B2-13 (SEQ ID NO: 65)	2xTr/Th	yes	LQSSGTEVDR GNQQHDTNDR DFTHTPLSS A
B2-14	2xTr/Th	yes	LQSSG5VAQG SSASVDVTAT NAVLSADSL SLGGGEPA (SEQ ID NO: 66)
B2-22	2xTr/Th	yes	LQSSGGAVAV TPGPVLSSA (SEQ ID NO: 67)
B2-23	2xTr/Th	yes	LQSSGHCRGK PVLCTHTA (SEQ ID NO: 68)
B2-15	2xTr/Th	yes	LQSSGVRPA (SEQ ID NO: 69)
B2-17	2xTr/Th	yes	no insert, Barnase & p3 in frame
B2-20,21	2xTr/Th	yes	no insert, Barnase & p3 in frame
B2-16,24	2xTr/Th	yes	LQSSGEPAPA HEAKPTEAPV AKAEAKPETP AHLSSA (SEQ ID NO: 70)
B2-18	2xTr/Th	no	LQSSGCVRLK RTSVNHQPDA WPEPHLKAAC EPA (SEQ ID NO: 71)
B2-19	2xTr/Th	no	LQSSGVVDWA KMREIADSIG AYLFVDMAHV AALSSA (SEQ ID NO: 72) --

- Replace the paragraph at page 47, lines 8-10 with the following replacement paragraph:

-- **Figure 2. The phagemid vectors pK1 and pK2.** These vectors contain a protease cleavable sequence between D2 and D3 of the phage p3 protein. In pK1, D2 + D3 are in frame; in pK2, D3 is out of frame. Nucleotide and amino acid sequence for the polylinker regions are shown for pK1 (SEQ ID NO: 73 and SEQ ID NO: 74, respectively) and pK2 (SEQ ID NO: 75 and SEQ ID NO: 76, respectively). --

- Replace the paragraph at page 47, lines 21-23 with the following replacement paragraph. Please note that number "43" was presented in brackets in the originally filed application. The brackets are replaced with parentheses herein.

-- Figure 5. The fd vector fd-3. The gene for the H102A mutant of Barnase is introduced by subcloning into fd-DOG (43) after PCR amplification with suitable oligonucleotides using the

restriction sites ApaLI (at the Barnase 5' end) and NotI to create fd-3. The nucleotide and amino acid sequence of the junction between Barnase and p3 sequences is shown in expanded view (SEQ ID NO 77 and SEQ ID NO: 78, respectively).--

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APPLICATION NO.	FILING DATE	FIRST NAMED INVENTOR	ATTORNEY DOCKET NO.	CONFIRMATION NO.
09/710,444	11/10/2000	Lutz Riechmann	8654/1090	5253

7590 02/27/2002

Palmer & Dodge LLP
One Beacon Street
Boston, MA 02109-3190

EXAMINER
CELSA, BENNETT M

ART UNIT	PAPER NUMBER
1627	

DATE MAILED: 02/27/2002

Please find below and/or attached an Office communication concerning this application or proceeding.

Docket # Doreen
Response due Notice to Comply
Statutory period 3/27/02 (8/27/02)
Palmer & Dodge LLP Drop Dead Date
Patent Department

UNITED STATES DEPARTMENT OF COMMERCE
Patent and Trademark Office
COMMISSIONER OF PATENTS AND TRADEMARKS
Washington, D.C. 20231

SERIAL NUMBER	FILING DATE	FIRST NAMED APPLICANT	ATTORNEY DOCKET NO.
09/ 710,444			

EXAMINER	
ART UNIT	PAPER NUMBER
1627	5

Please find below a communication from the EXAMINER in charge of this application

Sequence Rule Compliance: **NOTICE TO COMPLY**

This application fails to comply with the sequence rule quirements of 37 C.F.R. §§ 1.821-1.825 for the reason(s) set forth on the attached Notice To Comply With Requirements For Patent Applications Containing Nucleotide Sequence And/Or Amino Acid Sequence Disclosures. This application **encompasses sequences needing sequence identifiers (e.g. see pages 9, 15, 24, 30, 35, 36, 38, figures etc.).**

APPLICANT IS GIVEN 30 days FROM THE DATE OF THIS LETTER WITHIN WHICH TO COMPLY WITH THE SEQUENCE RULES, 37 C.R.F. §§ 1.821-1.825. Failure to comply with these requirements will result in ABANDONMENT of the application under 37 C.F.R. § 1.821(g). Extensions of time may be obtained by filing a petition accompanied by the extension fee under the provisions of 37 C.F.R. § 1.136. In no case may an applicant extend the period for response beyond the six month statutory period. Direct the response to the undersigned. Applicant is requested to return a copy of the attached Notice to Comply with the response.

Any inquiry concerning this communication or earlier communications from the examiner should be directed to Examiner Celsa whose telephone number is (703) 305-7556 If the examiner cannot be reached, inquiries can be directed to Supervisory Patent Examiner Venkat whose telephone number is (703) 308-0570. The fax number for the organization where this application or proceeding is assigned is (703) 308-4242. Any inquiry of a general nature or relating to the status of this application should be directed to the Group receptionist whose telephone number is (703) 308-0196.

Bennett Celsa (au 1627) (Feb. 25,2002)

BENNETT CELSA
PRIMARY EXAMINER

Application No. 09/710,444

NOTICE TO COMPLY WITH REQUIREMENTS FOR PATENT APPLICATIONS CONTAINING NUCLEOTIDE SEQUENCE AND/OR AMINO ACID SEQUENCE DISCLOSURES

The nucleotide and/or amino acid sequence disclosure contained in this application does not comply with the requirements for such a disclosure as set forth in 37 CFR 1.821 - 1.825 for the following reason(s):

☒ 1. This application clearly fails to comply with the requirements of 37 CFR 1.821 - 1.825. Applicant's attention is directed to these regulations, published at 1114 OG 29, May 15, 1990 and at 55 FR 18230, May 1, 1990.

☒ 2. This application does not contain, as a separate part of the disclosure on paper copy, a "Sequence Listing" as required by 37 CFR 1.821(c).

☒ 3. A copy of the "Sequence Listing" in computer readable form has not been submitted as required by 37 CFR 1.821

☐ 4. A copy of the "Sequence Listing" in computer readable form has been submitted. However, the content of the computer readable form does not comply with the requirements of 37 CFR 1.822 and/or 1.823, as indicated on the attached marked-up copy of the "Raw Sequence Listing."

☐ 5. The computer readable form that has been filed with this application has been found to be damaged and/or unreadable as indicated on the attached CRF Diskette Problem Report. A substitute computer readable form must be submitted as required by 37 CFR 1.825(d).

☐ 6. The paper copy of the "Sequence Listing" is not the same as the computer readable form of the "Sequence Listing" as required by 37 CFR 1.821(e).

☐ 7. Other: _____

Applicant must provide:

☒ An initial ~~or substitute~~ computer readable form (CRF) copy of the "Sequence Listing"

☒ An initial ~~or substitute~~ paper copy of the "Sequence Listing", as well as an amendment directing its entry into the specification

☒ A statement that the content of the paper and computer readable copies are the same and, where applicable, include no new matter, as required by 37 CFR 1.821(e) or 1.821(f) or 1.821(g) or 1.825(b) or 1.825(d)

For questions regarding compliance with these requirements, please contact:

For Rules Interpretation, call (703) 308-1123
For CRF submission help, call (703) 308-4212
For PatentIn software help, call (703) 308-6856

Please return a copy of this notice with your response.

Attachment for PTO-948 (Rev. 03/01, or earlier)
6/18/01

The below text replaces the pre-printed text under the heading, "Information on How to Effect Drawing Changes," on the back of the PTO-948 (Rev. 03/01, or earlier) form.

INFORMATION ON HOW TO EFFECT DRAWING CHANGES

1. Correction of Informalities – 37 CFR 1.85

New corrected drawings must be filed with the changes incorporated therein. Identifying indicia, if provided, should include the title of the invention, inventor's name, and application number, or docket number (if any) if an application number has not been assigned to the application. If this information is provided, it must be placed on the front of each sheet and centered within the top margin. If corrected drawings are required in a Notice of Allowability (PTOL-37), the new drawings **MUST** be filed within the **THREE MONTH** shortened statutory period set for reply in the Notice of Allowability. Extensions of time may NOT be obtained under the provisions of 37 CFR 1.136(a) or (b) for filing the corrected drawings after the mailing of a Notice of Allowability. The drawings should be filed as a separate paper with a transmittal letter addressed to the Official Draftsperson.

2. Corrections other than Informalities Noted by Draftsperson on form PTO-948.

All changes to the drawings, other than informalities noted by the Draftsperson, **MUST** be made in the same manner as above except that, normally, a highlighted (preferably red ink) sketch of the changes to be incorporated into the new drawings **MUST** be approved by the examiner before the application will be allowed. No changes will be permitted to be made, other than correction of informalities, unless the examiner has approved the proposed changes.

Timing of Corrections

Applicant is required to submit the drawing corrections within the time period set in the attached Office communication. See 37 CFR 1.85(a).

Failure to take corrective action within the set period will result in **ABANDONMENT** of the application.

SEQUENCE LISTING

<110> Riechmann, Lutz

Kristensen, Peter

Jestin, Jean-Luc

Winter, Gregory

<120> Selection System

<130> 8039/1090

<140> 09/710,444

<141> 2000-11-10

<150> GB 9810223.9

<151> 1998-05-13

<150> GB 9810228.8

<151> 1998-05-13

<150> PCT/GB99/01526

<151> 1999-05-13

<160> 78

<170> PatentIn version 3.1

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<212> PRT

<213> Artificial

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<223> Synthetic linker peptide sequence with protease recognition sites

<400> 1

Pro Ala Gly Leu Ser Glu Gly Ser Thr Ile Glu Gly Arg Gly Ala His

1 5 10 15

Glu

<210> 2

<211> 57

<212> DNA

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<223> Synthetic PCR primer for vector construction/screening

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<211> 89

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<210> 6

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<210> 8

<211> 24

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<222> (1)..(24)

<223> Synthetic PCR primer used to screen for recombinant clones

<400> 8

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<210> 9

<211> 26

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<221> misc_feature

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<210> 10

<211> 65

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<221> misc_feature

<222> (1)..(65)

<223> Synthetic PCR primer recognizing FLAG tag nucleotide sequence

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caaacgggcg gccgcagact acaaggatga cgacgacaag gaaactgttg aaagttgttt 60

agcaa 65

<210> 11

<211> 51

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<223> Synthetic PCT primer used to change codon usage in recombinant cl
ones

<400> 11

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<210> 12

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ones

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<211> 36

<212> DNA

<213> Artificial

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<223> Synthetic PCR primer for vector construction/screening

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ccctcggaac cggtacccca gctgcttcgt gggccc 36

<210> 14

<211> 47

<212> DNA

<213> Bacillus amyloliquefaciens

<400> 14

ctggcggcgg cccagccggc cctgcacagg ttatcaacac gtttgac 47

<210> 15

<211> 43

<212> DNA

<213> Bacillus amyloliquefaciens

<400> 15

ctcggaaccg gtacctctga tttttgtaaa ggtctgataa gcg 43

<210> 16

<211> 44

<212> DNA

<213> Gallus gallus

<400> 16

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<210> 17

<211> 41

<212> DNA

<213> Gallus gallus

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<211> 18

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<221> misc_feature

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<210> 19

<211> 17

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<220>

<221> misc_feature

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ctgcacctgg gccatgg 17

<210> 20

<211> 17

<212> DNA

<213> Artificial

<220>

<221> misc_feature

<222> (1)..(17)

<223> Synthetic PCR primer used for library construction

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<210> 21

<211> 126

<212> DNA

<213> Erwinia chrysanthemi

<220>

<221> misc_feature

<223> n at positions 23, 24, 29, 55, 56, 81, 97, 101, and 102 can be G, A, T or C

<220>

<221> misc_feature

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<223> n at position 23 can be G, A, T or C

<220>

<221> misc_feature

<222> (24)..(24)

<223> n at position 24 can be G, A, T or C

<220>

<221> misc_feature

<222> (29)..(29)

<223> n at position 29 can be G, A, T or C

<220>

<221> misc_feature

<222> (55)..(55)

<223> n at position 55 can be G, A, T or C

<220>

<221> misc_feature

<222> (56)..(56)

<223> n at position 56 can be G, A, T or C

<220>

<221> misc_feature

<222> (81)..(81)

<223> n at position 81 can be G, A, T or C

<220>

<221> misc_feature

<222> (97)..(97)

<223> n at position 97 can be G, A, T or C

<220>

<221> misc_feature

<222> (101)..(101)

<223> n at position 101 can be G, A, T or C

<220>

<221> misc_feature

<222> (102)..(102)

<223> n at position 102 can be G, A, T or C

<400> 21

gattacgcca agcttgcatg cannddctnt dtcaaggaga cagtcataat garrnnbcta 60

ttgsyaayrs yasyasyagb nttgttatta ctcsyanycv nncygdccat ggcccaggtg 120

cagctg 126

<210> 22

<211> 117

<212> DNA

<213> Bacteriophage M13mp18

<220>

<221> misc_feature

<222> (18)..(18)

<223> Nucleotide at position 18 can be G, A, T or C.

<220>

<221> misc_feature

<222> (19)..(19)

<223> Nucleotide at position 19 can be G, A, T or C.

<220>

<221> misc_feature

<222> (20)..(20)

<223> Nucleotide at position 20 can be G, A, T or C.

<220>

<221> misc_feature

<222> (21)..(21)

<223> Nucleotide at position 21 can be G, A, T or C.

<400> 22

gattacgcca agctttgnnn nctttttttww ggagattttc aacrtgaraa rattattatt 60

csyaattsyt ttagttsyts ytttctwtgy ggyccagccg gccatggccc aggtgca 117

<210> 23

<211> 18

<212> DNA

<213> Artificial sequence

<220>

<223> Synthetic PCR primer for vector construction

<400> 23

ctttatgctt ccggctcg 18

<210> 24

<211> 17

<212> DNA

<213> Artificial

<220>

<221> misc_feature

<222> (1)..(17)

<223> Synthetic PCT primer for library construction

<400> 24

cggccccatt cagatcc 17

<210> 25

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<213> Artificial

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<400> 25

aagcttgcat gcaaattcta tdtcaaggag acagttataa tgaaatacct 50

<210> 26

<211> 50

<212> DNA

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<222> (14)..(14)

<223> n at position 14 can be G, A, T or C.

<220>

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<222> (15)..(15)

<223> n at position 15 can be G, A, T or C.

<220>

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<222> (20)..(20)

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<222> (45)..(45)

<223> n at position 45 can be G, A, T or C.

<220>

<221> misc_feature

<222> (46)..(46)

<223> n at position 46 can be G, A, T or C.

<400> 26

aagcttgcat gcannddctn tdtcaaggag acagtcataa tgarrnnbct 50

<210> 27

<211> 50

<212> DNA

<213> Artificial

<220>

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<400> 27

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<210> 28

<211> 50

<212> DNA

<213> Artificial

<220>

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<223> Randomized E. chrysanthemi pelB sequence

<400> 28

aagcttgcat gcacgggctg tdtcaaggag acagtcataa tgagagggct 50

<210> 29

<211> 50

<212> DNA

<213> Artificial

<220>

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<222> (1)..(50)

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<400> 29

aagcttgcat gcaccagctc tdtcaaggag acagtcataa tgaggcggct 50

<210> 30

<211> 55

<212> DNA

<213> Artificial

<220>

<221> misc_feature

<222> (1)..(55)

<223> Randomized E. chrysanthemi pelB sequence

<400> 30

attcctaacg gcagccgctg gattgttatt actcgcggcc cagccggcca tggcc 55

<210> 31

<211> 55

<212> DNA

<213> artificial

<220>

<221> misc_feature

<222> (1)..(55)

<223> Randomized E. chrysanthemi pelB sequence

<220>

<221> misc_feature

<222> (22)..(22)

<223> n at position 22 can be G, A, T or C.

<220>

<221> misc_feature

<222> (38)..(38)

<223> n at position 38 can be G, A, T or C.

<220>

<221> misc_feature

<222> (42)..(42)

<223> n at position 42 can be G, A, T or C.

<220>

<221> misc_feature

<222> (43)..(43)

<223> n at position 43 can be G, A, T or C.

<400> 31

attgsyaayr syasyasyag bnttgttatt actcsyanyc vnncygdcca tggcc 55

<210> 32

<211> 55

<212> DNA

<213> Artificial

<220>

<221> misc_feature

<222> (1)..(55)

<223> Randomized E. chrysanthemi pelB sequence

<400> 32

attgcyaatg gtactgtyag gattgttatt actcccaccc ggtccgtcca tggcc 55

<210> 33

<211> 55

<212> DNA

<213> artificial

<220>

<221> misc_feature

<222> (1)..(55)

<223> Randomized E. chrysanthemi pelB sequence

<400> 33

attgcyaatg ctagtgcyag ggttgttatt actcccaatc gcgccggcca tggcc 55

<210> 34

<211> 54

<212> DNA

<213> Artificial

<220>

<221> misc_feature

<222> (1)..(54)

<223> Randomized E. chrysanthemi pelB sequence

<220>

<221> misc_feature

<222> (22)..(22)

<223> n at position 22 can be G, A, T or C.

<220>

<221> misc_feature

<222> (43)..(43)

<223> n at position 43 can be G, A, T or C.

<220>

<221> misc_feature

<222> (44)..(44)

<223> n at position 44 can be G, A, T or C.

<400> 34

attggtaata gcagcagtag bnttgttagg actcgcaccc ccnncyadcc atgg 54

<210> 35

<211> 22

<212> PRT

<213> Erwinia chrysanthemi

<400> 35

Met Lys Tyr Leu Leu Pro Thr Ala Ala Ala Gly Leu Leu Leu Leu Ala
1 5 10 15

Ala Gln Pro Ala Met Ala
20

<210> 36

<211> 22

<212> PRT

<213> Artificial

<220>

<221> MISC_FEATURE

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<223> Randomized E. chrysanthemi pelB sequence

<400> 36

Met Lys Thr Leu Ala Met Val Leu Val Gly Gly Pro Pro Gly Pro Ser
1 5 10 15

Ala Gln Pro Ala Met Ala
20

<210> 37
<211> 21
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<213> Artificial

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<223> Randomized E. chrysanthemi pelB sequence

<400> 37

Met Arg Gly Leu Ala Met Leu Val Ala Gly Gly Pro Ile Ala Pro Ala
1 5 10 15

Gln Pro Ala Met Ala

20

<210> 38

<211> 23

<212> PRT

<213> Artificial

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1 5 10 15

Pro Thr Gln Pro Ala Met Ala
20

<210> 39

<211> 50

<212> DNA

<213> Artificial

<220>

<221> misc_feature

<222> (1)..(50)

<223> Randomized bacteriophage M13 g3 sequence

<400> 39

aagctttgga cgctttttt tggagatttt caacgtgaaa aaattattat 50

<210> 40

<211> 50

<212> DNA

<213> Artificial

<220>

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<222> (9)..(9)

<223> n at position 9 is can be G, A, t or C.

<220>

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<222> (1)..(50)

<223> Randomized bacteriophage M13 g3 sequence

<220>

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<222> (10)..(10)

<223> n at position 10 is can be G, A, t or C.

<220>

<221> misc_feature

<222> (11)..(11)

<223> n at position 11 is can be G, A, t or C.

<220>

<221> misc_feature

<222> (12)..(12)

<223> n at position 12 is can be G, A, t or C.

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<210> 41

<211> 50

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<213> Artificial

<220>

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<222> (1)..(50)

<223> Randomized bacteriophage M13 g3 sequence.

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<210> 42

<211> 50

<212> DNA

<213> Artificial

<220>

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<222> (1)..(50)

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<213> Artificial

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<221> misc_feature

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<223> Randomized bacteriophage M13 g3 sequence

<400> 44

tcctaattcc tttagttgtt gctttctatg tggtccagcc ggccatggcc 50

<210> 45

<211> 22

<212> PRT

<213> Artificial

<220>

<221> MISC_FEATURE

<222> (1)..(22)

<223> Randomized bacteriophage M13 g3 sequence

<400> 45

Met Lys Lys Leu Leu Phe Ala Ile Pro Leu Val Val Pro Phe Tyr Ala
1 5 10 15

Ala Gln Pro Ala Met Ala
20

<210> 46

<211> 22

<212> PRT

<213> Artificial

<220>

<221> MISC_FEATURE

<222> (1)..(22)

<223> Randomized bacteriophage M13 g3 sequence

<400> 46

Met Arg Arg Leu Leu Leu Ala Pro Pro Val Ala Val Pro Phe Tyr Val
1 5 10 15

Val Gln Pro Ala Met Ala
20

<210> 47
<211> 18
<212> DNA
<213> artificial

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<222> (1)..(18)
<223> Synthetic oligonucleotide primer used as substrate for Stoffel fragment of Thermus aquaticus DNA polymerase I

<400> 47
tttcgcaaga tgtggcgt 18

<210> 48

<211> 12

<212> DNA

<213> Artificial

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<221> misc_feature

<222> (1)..(12)

<223> Synthetic primer used as substrate for Stoffel fragment of Thermu
s aquaticus DNA polymerase I

<400> 48

gcgaagatgt gg 12

<210> 49

<211> 30

<212> DNA

<213> artificial

<220>

<221> misc_feature

<222> (1)..(30)

<223> Synthetic oligonucleotide primer used as substrate for Thermus aq
uaticus DNA polymerase I

<400> 49

aaatacaaca ataaaacgcc acatcttgcg 30

<210> 50

<211> 20

<212> DNA

<213> Artificial

<220>

<221> misc_feature

<222> (1)..(20)

<223> Synthetic oligonucleotide sequence insert containing PstI restriction site and frame shift for H102A mutant barnase fusion construct fused to p3 gene of phage fd-3.

<400> 50

ctgcaggcgg tgcggccgca 20

<210> 51

<211> 24

<212> DNA

<213> artificial

<220>

<221> misc_feature

<222> (1)..(24)

<223> Synthetic oligonucleotide used for random priming

<220>

<221> misc_feature

<222> (19)..(19)

<223> n at position 19 can be G, A, T or C.

<220>

<221> misc_feature

<222> (20)..(20)

<223> n at position 20 can be G, A, T or C.

<220>

<221> misc_feature

<222> (21)..(21)

<223> n at position 21 can be G, A, T or C.

<220>

<221> misc_feature

<222> (22)..(22)

<223> n at position 22 can be G, A, T or C.

<220>

<221> misc_feature

<222> (23)..(23)

<223> n at position 23 can be G, A, T or C.

<220>

<221> misc_feature

<222> (24)..(24)

<223> n at position 24 can be G, A, T or C.

<400> 51

gagcctgcag agctcaggnn nnnn 24

<210> 52

<211> 23

<212> DNA

<213> artificial

<220>

<221> misc_feature

<222> (1)..(23)

<223> Synthetic PCR primer used to re-amplify randomly amplified E. coli genomic DNA sequences.

<400> 52

cgtgcgagcc tgcagagctc agg 23

<210> 53

<211> 45

<212> PRT

<213> artificial

<220>

<221> MISC_FEATURE

<222> (1)..(45)

<223> Barstar binding barnase-p3 fusion insert

<400> 53

Leu Gln Ser Ser Gly Asp Cys Val Ile Ser Asp Thr Cys Ile Ala Gly
1 5 10 15

Met Ala Glu Ala Ala Ala Cys Glu Glu Lys Phe Ser Ser Gln Asn Val
20 25 30

Gly Leu Thr Ile Thr Val Thr Pro Cys Leu Ser Ser Ala
35 40 45

<210> 54

<211> 44

<212> PRT

<213> artificial

<220>

<221> MISC_FEATURE

<222> (1)..(44)

<223> Barstar binding barnase-p3 fusion insert

<400> 54

Leu Gln Ser Ser Gly Cys Gly Ser Ser Gly Ser Ser Ile Asn Cys Leu
1 5 10 15

Pro Cys Gly Ala Thr Ser Arg Gly Thr Ser Pro Leu Ala Ser Gly Leu
20 25 30

Pro Ser Ser Ala Thr Ile His Cys Leu Ser Ser Ala
35 40

<210> 55

<211> 40

<212> PRT

<213> artificial

<220>

<221> MISC_FEATURE

<222> (1)..(40)

<223> Barstar binding barnase-p3 fusion insert

<400> 55

Leu Gln Ser Ser Gly Asp Ser Ala Gly Cys Lys Asn Met Thr Gly Gly
1 5 10 15

Arg Leu Tyr Ala His Thr Leu Glu Ala Ile Ile Pro Gly Phe Ala Val
20 25 30

Ser Ala Pro Ala Cys Glu Pro Ala
35 40

<210> 56

<211> 33

<212> PRT

<213> artificial

<220>

<221> MISC_FEATURE

<222> (1)..(33)

<223> Barstar binding barnase-p3 fusion insert

<400> 56

Leu Gln Ser Ser Gly Cys Val Arg Leu Lys Arg Thr Ser Val Asn His
1 5 10 15

Gln Pro Asp Ala Trp Pro Glu Pro His Leu Lys Ala Ala Cys Glu Pro
20 25 30

Ala

<210> 57

<211> 44

<212> PRT

<213> artificial

<220>

<221> MISC_FEATURE

<222> (1)..(44)

<223> Barstar binding barnase-p3 fusion insert

<400> 57

Leu Gln Ser Ser Gly Cys Gly Ser Ser Gly Ser Ser Ile Asn Cys Leu
1 5 10 15

Pro Cys Gly Ala Thr Ser Arg Gly Thr Ser Pro Leu Ala Ser Gly Leu
20 25 30

Pro Ser Ser Ala Thr Val Gln Cys Leu Ser Ser Ala
35 40

<210> 58

<211> 41

<212> PRT

<213> artificial

<220>

<221> MISC_FEATURE

<222> (1)..(41)

<223> Barstar binding barnase-p3 fusion insert

<400> 58

Leu Gln Ser Ser Gly Lys Ile Val Gln Ala Gly Ala Asn Ile Gln Asp
1 5 10 15

Gly Cys Ile Met His Gly Tyr Cys Asp Thr Asp Thr Ile Val Gly Glu
20 25 30

Asn Gly His Ile Gly Leu Ser Ser Ala
35 40

<210> 59
<211> 45
<212> PRT
<213> Artificial

<220>
<221> MISC_FEATURE
<222> (1)..(45)
<223> Barstar binding barnase-p3 fusion insert

<400> 59

Leu Gln Ser Ser Gly Val Cys Val Ile Ser Asp Thr Cys Ile Ala Gly

1 5 10 15

Thr Ala Glu Ala Ala Ala Cys Glu Glu Lys Phe Ser Ser Gln Asn Val
20 25 30

Gly His Thr Ile Thr Glu Thr Pro Cys Leu Ser Ser Ala
35 40 45

<210> 60

<211> 44

<212> PRT

<213> artificial

<220>

<221> MISC_FEATURE

<222> (1)..(44)

<223> Barstar binding barnase-p3 fusion insert

<400> 60

Leu Gln Ser Ser Gly Cys Gly Ser Ser Gly Ser Ser Ile Asn Cys Leu
1 5 10 15

Pro Cys Gly Ala Thr Ser Arg Gly Thr Ser Pro Leu Ala Ser Gly Leu
20 25 30

Pro Ser Ser Ala Thr Ile Gln Cys Leu Ser Ser Ala
35 40

<210> 61

<211> 53

<212> PRT

<213> Artificial

<220>

<221> MISC_FEATURE

<222> (1)..(53)

<223> Barstar binding barnase-p3 fusion insert

<400> 61

Leu Gln Ser Ser Gly Gln Asp Ser Gln Arg Glu His Ala Ser His Thr
1 5 10 15

Ala Glu Asp Asp Cys Glu Asp Gln Thr Arg Ile His Gln His Ile Arg
20 25 30

Glu Val Asp Phe Val Asp Thr Pro Gln Glu Val Asp Asp Cys Arg Ala
35 40 45

Ala Leu Ser Ser Ala
50

<210> 62
<211> 33
<212> PRT
<213> Artificial

<220>
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<222> (1)..(33)
<223> Barstar binding barnase-p3 fusion insert

<400> 62

Leu Gln Ser Ser Gly Cys Val Arg Leu Lys Arg Thr Ser Val Asn His
1 5 10 15

Gln Pro Asp Ala Trp Pro Glu Pro His Leu Lys Ala Ala Cys Glu Pro
20 25 30

Ala

<210> 63

<211> 9

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<222> (1)..(9)

<223> Barstar binding barnase-p3 fusion insert

<400> 63

Leu Gln Ser Ser Gly Val Arg Pro Ala
1 5

<210> 64

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<400> 64

Leu Gln Ser Ser Gly Cys Gly Ser Ser Gly Ser Ser Ile Asn Cys Leu
1 5 10 15

Pro Cys Gly Ala Thr Ser Arg Gly Thr Ser Pro Leu Ala Ser Gly Leu
20 25 30

Pro Ser Ser Ala Thr Ile Gln Cys Leu Ser Ser Ala
35 40

<210> 65

<211> 30

<212> PRT

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<220>

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<222> (1)..(30)

<223> Barstar binding barnase-p3 fusion insert

<400> 65

Leu Gln Ser Ser Gly Thr Glu Val Asp Arg Gly Asn Gln Gln His Asp
1 5 10 15

Thr Asn Asp Arg Asp Phe Thr His Thr Pro Leu Ser Ser Ala
20 25 30

<210> 66

<211> 36

<212> PRT

<213> Artificial

<220>

<221> MISC_FEATURE

<222> (1)..(36)

<223> Barstar binding barnase-p3 fusion insert

<400> 66

Leu Gln Ser Ser Gly Val Ala Gln Gly Ser Ser Ala Ser Val Asp Val
1 5 10 15

Thr Ala Thr Asn Ala Val Leu Ser Ala Asp Ser Leu Ser Leu Gly Gly

20 25 30

Gly Glu Pro Ala

35

<210> 67

<211> 19

<212> PRT

<213> Artificial

<220>

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<222> (1)..(19)

<223> Barstar binding barnase-p3 fusion insert

<400> 67

Leu Gln Ser Ser Gly Gly Ala Val Ala Val Thr Pro Gly Pro Val Leu

1 5 10 15

Ser Ser Ala

<210> 68

<211> 18

<212> PRT

<213> Artificial

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<222> (1)..(18)

<223> Barstar binding barnase-p3 fusion insert

<400> 68

Leu Gln Ser Ser Gly His Cys Arg Gly Lys Pro Val Leu Cys Thr His
1 5 10 15

Thr Ala

<210> 69

<211> 9

<212> PRT

<213> Artificial

<220>

<221> MISC_FEATURE

<222> (1)..(9)

<223> Barstar binding barnase-p3 fusion insert

<400> 69

Leu Gln Ser Ser Gly Val Arg Pro Ala

1 5

<210> 70

<211> 36

<212> PRT

<213> Artificial

<220>

<221> MISC_FEATURE

<222> (1)..(36)

<223> Barstar binding barnase-p3 fusion insert

<400> 70

Leu Gln Ser Ser Gly Glu Pro Ala Pro Ala His Glu Ala Lys Pro Thr

1 5 10 15

Glu Ala Pro Val Ala Lys Ala Glu Ala Lys Pro Glu Thr Pro Ala His
20 25 30

Leu Ser Ser Ala
35

<210> 71

<211> 33

<212> PRT

<213> Artificial

<220>

<221> MISC_FEATURE

<222> (1)..(33)

<223> Barstar binding barnase-p3 fusion insert

<400> 71

Leu Gln Ser Ser Gly Cys Val Arg Leu Lys Arg Thr Ser Val Asn His
1 5 10 15

Gln Pro Asp Ala Trp Pro Glu Pro His Leu Lys Ala Ala Cys Glu Pro

20 25 30

Ala

<210> 72

<211> 36

<212> PRT

<213> Artificial

<220>

<221> MISC_FEATURE

<222> (1)..(36)

<223> Barstar binding barnase-p3 fusion insert

<400> 72

Leu Gln Ser Ser Gly Val Val Asp Trp Ala Lys Met Arg Glu Ile Ala
1 5 10 15

Asp Ser Ile Gly Ala Tyr Leu Phe Val Asp Met Ala His Val Ala Ala
20 25 30

Leu Ser Ser Ala

35

<210> 73

<211> 117

<212> DNA

<213> Artificial

<220>

<221> misc_feature

<222> (1)..(117)

<223> Vector pK1 polylinker sequence

<400> 73

aatgctggcg gcggcccagc cggcctttct gaggggtcga ctatagaagg acgaggggcc 60

cacgaaggag gtggggtacc cggttccgag ggtggttccg gttccggtga ttttgat 117

<210> 74

<211> 39

<212> PRT

<213> Artificial

<220>

<221> MISC_FEATURE

<222> (1)..(39)

<223> Polypeptide encoded by pK1 vector polylinker sequence

<400> 74

Asn Ala Gly Gly Gly Pro Ala Gly Leu Ser Glu Gly Ser Thr Ile Glu
1 5 10 15

Gly Arg Gly Ala His Glu Gly Gly Gly Val Pro Gly Ser Glu Gly Gly
20 25 30

Ser Gly Ser Gly Asp Phe Asp
35

<210> 75

<211> 117

<212> DNA

<213> Artificial

<220>

<221> misc_feature

<222> (1)..(117)

<223> vector pK2 polylinker sequence

<400> 75

aatgctggcg gcggcccagc cggcctttct gaggggtcga ctatagaagg acgagggccc 60

acgaagcagc tggggtaccg gttccgaggg tggttccggt tccggtgatt ttgatta 117

<210> 76

<211> 39

<212> PRT

<213> Artificial

<220>

<221> MISC_FEATURE

<222> (1)..(39)

<223> Polypeptide sequence encoded by vector pK2 polylinker region.

<220>

<221> MISC_FEATURE

<222> (38)..(38)

<223> X represents a TGA stop codon

<220>

<221> MISC_FEATURE

<222> (36)..(36)

<223> X represents a stop codon (TGA)

<400> 76

Asn Ala Gly Gly Gly Pro Ala Gly Leu Ser Glu Gly Ser Thr Ile Glu
1 5 10 15

Gly Arg Gly Pro Thr Lys Gln Leu Gly Tyr Arg Phe Arg Gly Trp Phe
20 25 30

Arg Phe Arg Xaa Phe Xaa Leu
35

<210> 77

<211> 35

<212> DNA

<213> Artificial

<220>

<221> misc_feature

<222> (1)..(35)

<223> Sequence of the junction region between Barnase and p3 in recombi
nant fusion vector fd-3.

<400> 77

atcagactgc aggcggtgcg gccgcagaaa ctgtt 35

<210> 78

<211> 11

<212> PRT

<213> artificial

<220>

<221> MISC_FEATURE

<222> (1)..(11)

<223> Amino acid sequence about the junction of barnase and p3 coding r
egions of recombinant fusion vector fd-3.

<400> 78

Ile Arg Leu Gln Ala Ala Ala Ala Glu Thr Val
1 5 10

1

1

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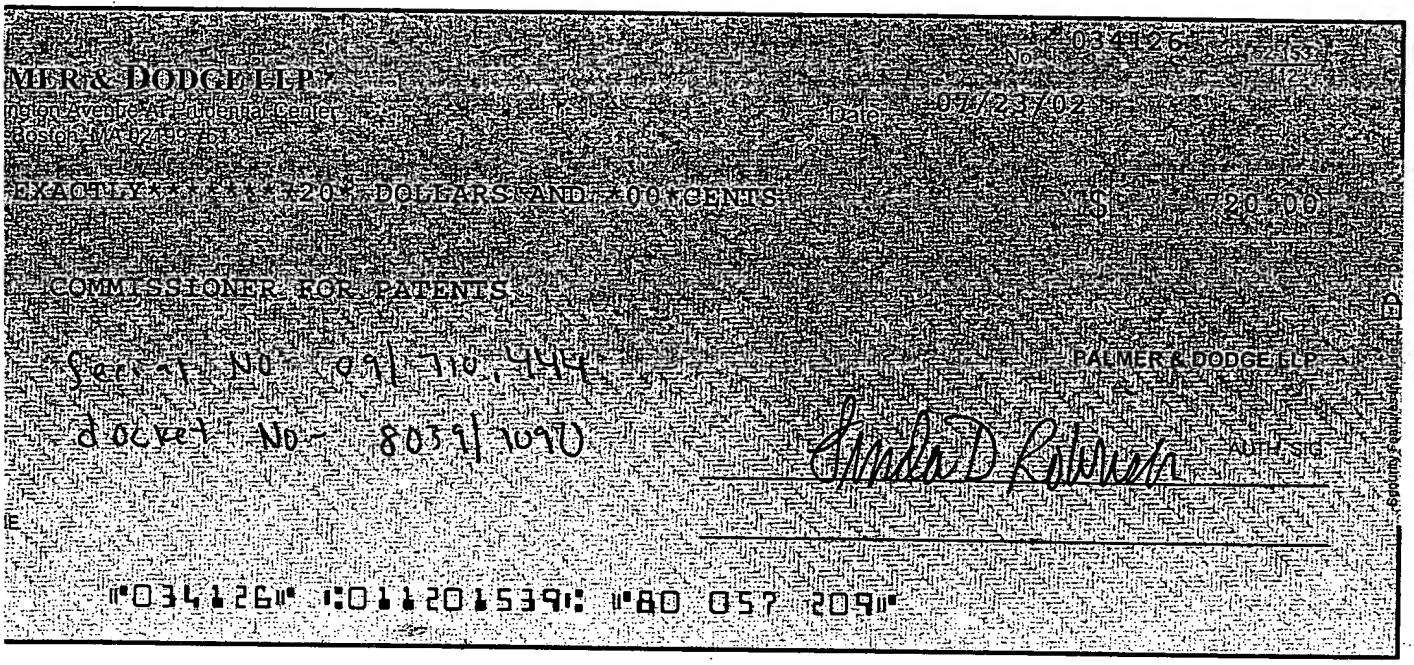

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Applicant(s): Riechmann et al.

Title: "Selection System"

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